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(54) G-CSF analog compositions and methods

. G-CSF Analoge und Verfahren zu ihrer Herstellung

Analogues de G-CSF et méthodes pour les obtenir

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Description

Field of the Invention

[0001] This invention relates to granulocyte colony stimulating factor ("G-CSF") analogs.

Background

[0002] Hematopoiesis is controlled by two systems: the cells within the bone marrow microenvironment and growth factors. The growth factors, also called colony stimulating factors, stimulate committed progenitor cells to proliferate and to form colonies of differentiating blood cells. One of these factors is granulocyte colony stimulating factor, herein called G-CSF, which preferentially stimulates the growth and development of neutrophils, indicating a potential use in neutropenic states. Welte et al., PNAS-USA 82: 1526-1530 (1985); Souza et al., Science 232: 61-65 (1986) and Gabrilove, J. Seminars in Hematology 26: (2) 1-14 (1989).

[0003] In humans, endogenous G-CSF is detectable in blood plasma. Jones et al., Bailliere's Clinical Hematology 2 (1): 83-111 (1989). G-CSF is produced by fibroblasts, macrophages, T cells trophoblasts, expression product of a single copy gene comprised of four exons and five introns located on chromosome seventeen. Transcription of this locus produces a mRNA species which is differentially processed, resulting in two forms of G-CSF mRNA, one version coding for a protein of 177 amino acids, the other coding for a protein of 174 amino acids, Nagata et al., EMBO J 5: 575-581 (1986), and the form comprised of 174 amino acids has been found to have the greatest specific in vivo biological activity. G-CSF is species cross-reactive, such that when human G-CSF is administered to another mammal such as a mouse, canine or monkey, sustained neutrophil leukocytosis is elicited. Moore et al., PNAS-USA 84: 7134-7138 (1987).

[0004] Human G-CSF can be obtained and purified from a number of sources. Natural human G-CSF (nhG-CSF) can be isolated from the supernatants of cultured human tumor cell lines. The development of recombinant DNA technology, see, for instance, U.S. Patent 4,810,643 (Souza) incorporated herein by reference, has enabled the production of commercial scale quantities of G-CSF in glycosylated form as a product of eukaryotic host cell expression, and of G-CSF in non-glycosylated form as a product of prokaryotic host cell expression.

[0005] G-CSF has been found to be useful in the treatment of indications where an increase in neutrophils will provide benefits. For example, for cancer patients, G-CSF is beneficial as a means of selectively stimulating neutrophil production to compensate for hematopoietic deficits resulting from chemotherapy or radiation therapy. Other indications include treatment of various infectious diseases and related conditions, such as sepsis, which is typically caused by a metabolite of bacteria. G-CSF is also useful alone, or in combination with other compounds, such as other cytokines, for growth or expansion of cells in culture, for example, for bone marrow transplants.

[0006] Signal transduction, the way in which G-CSF effects cellular metabolism, is not currently thoroughly understood. G-CSF binds to a cell-surface receptor which apparently initiates the changes within particular progenitor cells, leading to cell differentiation.

[0007] Various altered G-CSF's have been reported. Generally, for design of drugs, certain changes are known to have certain structural effects. For example, deleting one cysteine could result in the unfolding of a molecule which is, in its unaltered state, is normally folded via a disulfide bridge. There are other known methods for adding, deleting or substituting amino acids in order to change the function of a protein.

[0008] Recombinant human G-CSF mutants have been prepared, but the method of preparation does not include overall structure/function relationship information. For example, the mutation and biochemical modification of Cys 18 has been reported. Kuga et al., Biochem. Biophy. Res. Comm 159: 103-111 (1989); Lu et al., Arch. Biochem. Biophys. 268: 81-92 (1989).

[0009] In U.S. Patent No. 4, 810, 643, entitled, "Production of Pluripotent Granulocyte Colony-Stimulating Factor" (as cited above), polypeptide analogs and peptide fragments of G-CSF are disclosed generally. Specific G-CSF analogs disclosed include those with the cysteins at positions 17, 36, 42, 64, and 74 (of the 174 amino acid species or of those having 175 amino acids, the additional amino acid being an N-terminal methionine) substituted with another amino acid, (such as serine), and G-CSF with an alanine in the first (N-terminal) position.

[0010] EP 0 335 423 entitled "Modified human G-CSF" reportedly discloses the modification of at least one amino group in a polypeptide having hG-CSF activity.

[0011] EP 0 272 703 entitled "Novel Polypeptide" reportedly discloses G-CSF derivatives having an amino acid substituted or deleted at or "in the neighborhood" of the N terminus.

[0012] EP 0 459 630, entitled "Polypeptides" reportedly discloses derivatives of naturally occurring G-CSF having at least one of the biological properties of naturally occurring G-CSF and a solution stability of at least 35% at 5 mg/ml in which the derivative has at least Cys^{17} of the native sequence replaced by a Ser^{17} residue and Asp^{27} of the native sequence replaced by a Ser^{27} residue.

[0013] EP 0 256 843 entitled "Expression of G-CSF and Muteins Thereof and Their Uses" reportedly discloses a

modified DNA sequence encoding G-CSF wherein the N-terminus is modified for enhanced expression of protein in recombinant host cells, without changing the amino acid sequence of the protein.

[0014] EP 0 243 153 entitled "Human G-CSF Protein Expression" reportedly discloses G-CSF to be modified by inactivating at least one yeast KEX2 protease processing site for increased yield in recombinant production using yeast.

[0015] Shaw, U.S. Patent No. 4,904,584, entitled "Site-Specific Homogeneous Modification of Polypeptides," reportedly discloses lysine altered proteins.

[0016] WO/9012874 reportedly discloses cysteine altered variants of proteins.

[0017] Australian patent application Document No. AU-A-10948/92, entitled, "Improved Activation of Recombinant Proteins" reportedly discloses the addition of amino acids to either terminus of a G-CSF molecule for the purpose of aiding in the folding of the molecule after prokaryotic expression.

[0018] Australian patent application Document No. AU-A-76380/91, entitled, "Muteins of the Granulocyte Colony Stimulating Factor (G-CSF)" reportedly discloses muteins of the granulocyte stimulating factor G-CSF in the sequence Leu-Gly-His-Ser-Leu-Gly-Ile at position 50-56 of G-CSF with 174 amino acids, and position 53 to 59 of the G-CSF with 177 amino acids, or/and at least one of the four histadine residues at positions 43, 79, 156 and 170 of the mature G-CSF with 174 amino acids or at positions 46, 82, 159, or 173 of the mature G-CSF with 177 amino acids.

[0019] GB 2 213 821, entitled "Synthetic Human Granulocyte Colony Stimulating Factor Gene" reportedly discloses a synthetic G-CSF-encoding nucleic acid sequence incorporating restriction sites to facilitate the cassette mutagenesis of selected regions, and flanking restriction sites to facilitate the incorporation of the gene into a desired expression system.

[0020] G-CSF has reportedly been crystallized to some extent, e.g., EP 344 796, and the overall structure of G-CSF has been surmised, but only on a gross level. Bazan, Immunology Today 11: 350-354 (1990); Parry et al., J. Molecular Recognition 8: 107-110 (1988). To date, there have been no reports of the overall structure of G-CSF, and no systematic studies of the relationship of the overall structure and function of the molecule, studies which are essential to the systematic design of G-CSF analogs. Accordingly, there exists a need for a method of this systematic design of G-CSF analogs, and the resultant compositions.

Summary of the Invention

[0021] The three dimensional structure of G-CSF has now been determined to the atomic level. From this three-dimensional structure, one can now forecast with substantial certainty how changes in the composition of a G-CSF molecule may result in structural changes. These structural characteristics may be correlated with biological activity to design and produce G-CSF analogs.

[0022] Although others had speculated regarding the three dimensional structure of G-CSF, Bazan, Immunology Today 11: 350-354 (1990); Parry et al., J. Molecular Recognition 8: 107-110 (1988), these speculations were of no help to those wishing to prepare G-CSF analogs either because the surmised structure was incorrect (Parry et al., supra) and/or because the surmised structure provided no detail correlating the constituent moieties with structure. The present determination of the three-dimensional structure to the atomic level is by far the most complete analysis to date, and provides important information to those wishing to design and prepare G-CSF analogs. For example, from the present three dimensional structural analysis, precise areas of hydrophobicity and hydrophilicity have been determined.

[0023] Relative hydrophobicity is important because it directly relates to the stability of the molecule. Generally, biological molecules, found in aqueous environments, are externally hydrophilic and internally hydrophobic; in accordance with the second law of thermodynamics provides, this is the lowest energy state and provides for stability. Although one could have speculated that G-CSF's internal core would be hydrophobic, and the outer areas would be hydrophilic, one would have had no way of knowing specific hydrophobic or hydrophilic areas. With the presently provided knowledge of areas of hydrophobicity/philicity, one may forecast with substantial certainty which changes to the G-CSF molecule will affect the overall structure of the molecule.

[0024] As a general rule, one may use knowledge of the geography of the hydrophobic and hydrophilic regions to design analogs in which the overall G-CSF structure is not changed, but change does affect biological activity ("biological activity" being used here in its broadest sense to denote function). One may correlate biological activity to structure. If the structure is not changed, and the mutation has no effect on biological activity, then the mutation has no biological function. If, however, the structure is not changed and the mutation does affect biological activity, then the residue (or atom) is essential to at least one biological function. Some of the present working examples were designed to provide no change in overall structure, yet have a change in biological function.

[0025] Based on the correlation of structur to biological activity, the present invention relates to G-CSF analogs. These analogs are molecules which have more, fewer, different or modified amino acid residues from the G-CSF amino acid sequence. The modifications may be by addition, substitution, or deletion of one or more amino acid residues. The modification may include the addition or substitution of analogs of the amino acids themselves, such as peptidomimetics or amino acids with altered moieties such as altered side groups. The G-CSF used as a basis for comparison may

be of human, animal or recombinant nucleic acid-technology origin (although the working examples disclosed herein are based on the recombinant production of the 174 amino acid species of human G-CSF, having an extra N-terminus methionyl residue). The analogs may possess functions different from natural human G-CSF molecule, or may exhibit the same functions, or varying degrees of the same functions. For example, the analogs may be designed to have a higher or lower biological activity, have a longer shelf-life or a decrease in stability, be easier to formulate, or more difficult to combine with other ingredients. The analogs may have no hematopoietic activity, and may therefore be useful as an antagonist against G-CSF effect (as, for example, in the overproduction of G-CSF). From time to time herein the present analogs are referred to as proteins or peptides for convenience, but contemplated herein are other types of molecules, such as peptidomimetics or chemically modified peptides.

[0026] In another aspect, the present disclosure relates to related compositions containing a G-CSF analog as an active ingredient. The term, "related composition," as used herein, is meant to denote a composition which may be obtained once the identity of the G-CSF analog is ascertained (such as a G-CSF analog labeled with a detectable label, related receptor or pharmaceutical composition). Also considered a related composition are chemically modified versions of the G-CSF analog, such as those having attached at least one polyethylene glycol molecule.

[0027] For example, one may prepare a G-CSF analog to which a detectable label is attached, such as a fluorescent, chemiluminescent or radioactive molecule.

[0028] Another example is a pharmaceutical composition which may be formulated by known techniques using known materials, see, e.g., Remington's Pharmaceutical Sciences, 18th Ed. (1990, Mack Publishing Co., Easton, Pennsylvania 18042) pages 1435-1712, which are herein incorporated by reference. Generally, the formulation will depend on a variety of factors such as administration, stability, production concerns and other factors. The G-CSF analog may be administered by injection or by pulmonary administration via inhalation. Enteric dosage forms may also be available for the present G-CSF analog compositions, and therefore oral administration may be effective. G-CSF analogs may be inserted into liposomes or other microcarriers for delivery, and may be formulated in gels or other compositions for sustained release. Although preferred compositions will vary depending on the use to which the composition will be put, generally, for G-CSF analogs having at least one of the biological activities of natural G-CSF, preferred pharmaceutical compositions are those prepared for subcutaneous injection or for pulmonary administration via inhalation, although the particular formulations for each type of administration will depend on the characteristics of the analog.

[0029] Another example of related composition is a receptor for the present analog. As used herein, the term "receptor" indicates a moiety which selectively binds to the present analog molecule. For example, antibodies, or fragments thereof, or "recombinant antibodies" (see Huse et al., Science 246:1275 (1989)) may be used as receptors. Selective binding does not mean only specific binding (although binding-specific receptors are encompassed herein), but rather that the binding is not a random event. Receptors may be on the cell surface or intra- or extra-cellular, and may act to effectuate, inhibit or localize the biological activity of the present analogs. Receptor binding may also be a triggering mechanism for a cascade of activity indirectly related to the analog itself. Also contemplated herein are nucleic acids, vectors containing such nucleic acids and host cells containing such nucleic acids which encode such receptors.

[0030] Another example of a related composition is a G-CSF analog with a chemical moiety attached. Generally, chemical modification may alter biological activity or antigenicity of a protein, or may alter other characteristics, and these factors will be taken into account by a skilled practitioner. As noted above, one example of such chemical moiety is polyethylene glycol. Modification may include the addition of one or more hydrophilic or hydrophobic polymer molecules, fatty acid molecules, or polysaccharide molecules. Examples of chemical modifiers include polyethylene glycol, alkIpolyethylene glycols, DI-poly(amino acids), polyvinylpyrrolidone, polyvinyl alcohol, pyran copolymer, acetic acid/acylation, proprionic acid, palmitic acid, stearic acid, dextran, carboxymethyl cellulose, pullulan, or agarose. See, Francis, *Focus on Growth Factors* 3: 4-10 (May 1992) (published by Mediscript, Mountview Court, Friern Barnet Lane, London N20 OLD, UK). Also, chemical modification may include an additional protein or portion thereof, use of a cytotoxic agent, or an antibody. The chemical modification may also include lecithin.

[0031] In another aspect, the present disclosure relates to nucleic acids encoding such analogs. The nucleic acids may be DNAs or RNAs or derivatives thereof, and will typically be cloned and expressed on a vector, such as a phage or plasmid containing appropriate regulatory sequences. The nucleic acids may be labeled (such as using a radioactive, chemiluminescent, or fluorescent label) for diagnostic or prognostic purposes, for example. The nucleic acid sequence may be optimized for expression, such as including codons preferred for bacterial expression. The nucleic acid and its complementary strand, and modifications thereof which do not prevent encoooding of the desired analog are here contemplated.

[0032] In another aspect, the present disclosure relates to host cells containing the above nucleic acids encoding the present analogs. Host cells may be eukaryotic or prokaryotic, and expression systems may include extra steps relating to the attachment (or prevention) of sugar groups (glycosylation), proper folding of the molecule, the addition or deletion of leader sequences or other factors incident to recombinant expression.

[0033] In another aspect the present disclosure relates to antisense nucleic acids which act to prevent or modify the

type or amount of expression of such nucleic acid sequences. These may be prepared by known methods.

[0034] In another aspect of the present disclosure, the nucleic acids encoding a present analog may be used for gene therapy purposes, for example, by placing a vector containing the analog-encoding sequence into a recipient so the nucleic acid itself is expressed inside the recipient who is in need of the analog composition. The vector may first be placed in a carrier, such as a cell, and then the carrier placed into the recipient. Such expression may be localized or systemic. Other carriers include non-naturally occurring carriers, such as liposomes or other microcarriers or particles, which may act to mediate gene transfer into a recipient.

[0035] The present disclosure also provides for computer programs for the expression (such as visual display) of the G-CSF or analog three dimensional structure, and further, a computer program which expresses the identity of each constituent of a G-CSF molecule and the precise location within the overall structure of that constituent, down to the atomic level. Set forth below is one example of such program. There are many currently available computer programs for the expression of the three dimensional structure of a molecule. Generally, these programs provide for inputting of the coordinates for the three dimensional structure of a molecule (i.e., for example, a numerical assignment for each atom of a G-CSF molecule along an x, y, and z axis), means to express (such as visually display) such coordinates, means to alter such coordinates and means to express an image of a molecule having such altered coordinates. One may program crystallographic information, i.e., the coordinates of the location of the atoms of a G-CSF molecule in three dimension space, wherein such coordinates have been obtained from crystallographic analysis of said G-CSF molecule, into such programs to generate a computer program for the expression (such as visual display) of the G-CSF three dimensional structure. Also provided, therefore, is a computer program for the expression of G-CSF analog three dimensional structure. Preferred is the computer program Insight II, version 4, available from Biosym, San Diego, California, with the coordinates as set forth in FIGURE 5 input. Preferred expression means is on a Silicon Graphics 320 VGX computer, with Crystal Eyes glasses (also available from Silicon Graphics), which allows one to view the G-CSF molecule or its analog stereoscopically. Alternatively, the present G-CSF crystallographic coordinates and diffraction data are also deposited in the Protein Data Bank, Chemistry Department, Brookhaven National Laboratory, Upton, New York 119723, USA. One may use these data in preparing a different computer program for expression of the three dimensional structure of a G-CSF molecule or analog thereof. Therefore, another aspect of the present invention is a computer program for the expression of the three dimensional structure of a G-CSF molecule. Also provided is said computer program for visual display of the three dimensional structure of a G-CSF molecule; and further, said program having means for altering such visual display. Apparatus useful for expression of such computer program, particularly for the visual display of the computer image of said three dimensional structure of a G-CSF molecule or analog thereof is also therefore here provided, as well as means for preparing said computer program and apparatus.

[0036] The computer program is useful for preparation of G-CSF analogs because one may select specific sites on the G-CSF molecule for alteration and readily ascertain the effect the alteration will have on the overall structure of the G-CSF molecule. Selection of said site for alteration will depend on the desired biological characteristic of the G-CSF analog. If one were to randomly change said G-CSF molecule (r-met-hu-G-CSF) there would be 175^{20} possible substitutions, and even more analogs having multiple changes, additions or deletions. By viewing the three dimensional structure wherein said structure is correlated with the composition of the molecule, the selection for sites of alteration is no longer a random event, but sites for alteration may be determined rationally.

[0037] As set forth above, identity of the three dimensional structure of G-CSF, including the placement of each constituent down to the atomic level has now yielded information regarding which moieties are necessary to maintain the overall structure of the G-CSF molecule. One may therefore select whether to maintain the overall structure of the G-CSF molecule when preparing a G-CSF analog of the present invention, or whether (and how) to change the overall structure of the G-CSF molecule when preparing a G-CSF analog of the present invention. Optionally, once one has prepared such analog, one may test such analog for a desired characteristic.

[0038] One may, for example, seek to maintain the overall structure possessed by a non-altered natural or recombinant G-CSF molecule. The overall structure is presented in Figures 2, 3, and 4, and is described in more detail below. Maintenance of the overall structure may ensure receptor binding, a necessary characteristic for an analog possessing the hematopoietic capabilities of natural G-CSF (if no receptor binding, signal transduction does not result from the presence of the analog). It is contemplated that one class of G-CSF analogs will possess the three dimensional core structure of a natural or recombinant (non-altered) G-CSF molecule, yet possess different characteristics, such as an increased ability to selectively stimulate neutrophils. Another class of G-CSF analogs are those with a different overall structure which diminishes the ability of a G-CSF analog molecule to bind to a G-CSF receptor, and possesses a diminished ability to selectively stimulate neutrophils as compared to non-altered natural or recombinant G-CSF.

[0039] For example, it is now known which moieties within the internal regions of the G-CSF molecule are hydrophobic, and, correspondingly, which moieties on the external portion of the G-CSF molecule are hydrophilic. Without knowledge of the overall three dimensional structure, preferably to the atomic level as provided herein, one could not forecast which alterations within this hydrophobic internal area would result in a change in the overall structural conformation of the molecule. An overall structural change could result in a functional change, such as lack of receptor bind-

ing, for example, and therefore, diminishment of biological activity as found in non-altered G-CSF. Another class of G-CSF analogs is therefore G-CSF analogs which possess the same hydrophobicity as (non-altered) natural or recombinant G-CSF. More particularly, another class of G-CSF analogs possesses the same hydrophobic moieties within the four helical bundle of its internal core as those hydrophobic moieties possessed by (non-altered) natural or recombinant G-CSF yet have a composition different from said non-altered natural or recombinant G-CSF.

[0040] Another example relates to external loops which are structures which connect the internal core (helices) of the G-CSF molecule. From the three dimensional structure -- including information regarding the spatial location of the amino acid residues -- one may forecast that certain changes in certain loops will not result in overall conformational changes. Therefore, another class of G-CSF analogs provided herein is that having an altered external loop but possessing the same overall structure as (non-altered) natural or recombinant G-CSF. More particularly, another class of G-CSF analogs provided herein are those having an altered external loop, said loop being selected from the loop present between helices A and B; between helices B and C; between helices C and D; between helices D and A, as those loops and helices are identified herein. More particularly, said loops, preferably the AB loop and/or the CD loop are altered to increase the half life of the molecule by stabilizing said loops. Such stabilization may be by connecting all or a portion of said loop(s) to a portion of an alpha helical bundle found in the core of a G-CSF (or analog) molecule. Such connection may be via beta sheet, salt bridge, disulfide bonds, hydrophobic interaction or other connecting means available to those skilled in the art, wherein such connecting means serves to stabilize said external loop or loops. For example, one may stabilize the AB or CD loops by connecting the AB loop to one of the helices within the internal region of the molecule.

[0041] The N-terminus also may be altered without change in the overall structure of a G-CSF molecule, because the N-terminus does not effect structural stability of the internal helices, and, although the external loops are preferred for modification, the same general statements apply to the N-terminus.

[0042] Additionally, such external loops may be the site(s) for chemical modification because in (non-altered) natural or recombinant G-CSF such loops are relatively flexible and tend not to interfere with receptor binding. Thus, there would be additional room for a chemical moiety to be directly attached (or indirectly attached via another chemical moiety which serves as a chemical connecting means). The chemical moiety may be selected from a variety of moieties available for modification of one or more function of a G-CSF molecule. For example, an external loop may provide sites for the addition of one or more polymer which serves to increase serum half-life, such as a polyethylene glycol molecule. Such polyethylene glycol molecule(s) may be added wherein said loop is altered to include additional lysines which have reactive side groups to which polyethylene glycol moieties are capable of attaching. Other classes of chemical moieties may also be attached to one or more external loops, including but not limited to other biologically active molecules, such as receptors, other therapeutic proteins (such as other hematopoietic factors which would engender a hybrid molecule), or cytotoxic agents (such as diphtheria toxin). This list is of course not complete; one skilled in the art possessed of the desired chemical moiety will have the means to effect attachment of said desired moiety to the desired external loop. Therefore, another class of the present G-CSF analogs includes those with at least one alteration in an external loop wherein said alteration provides for the addition of a chemical moiety such as at least one polyethylene glycol molecule.

[0043] Deletions, such as deletions of sites recognized by proteins for degradation of the molecule, may also be effectual in the external loops. This provides alternative means for increasing half-life of a molecule otherwise having the G-CSF receptor binding and signal transduction capabilities (i.e., the ability to selectively stimulate the maturation of neutrophils). Therefore, another class of the present G-CSF analogs includes those with at least one alteration in an external loop wherein said alteration decreases the turnover of said analog by proteases. Preferred loops for such alterations are the AB loop and the CD loop. One may prepare an abbreviated G-CSF molecule by deleting a portion of the amino acid residues found in the external loops (identified in more detail below), said abbreviated G-CSF molecule may have additional advantages in preparation or in biological function.

[0044] Another example relates to the relative charges between amino acid residues which are in proximity to each other. As noted above, the G-CSF molecule contains a relatively tightly packed four helical bundle. Some of the faces on the helices face other helices. At the point (such as a residue) where a helix faces another helix, the two amino acid moieties which face each other may have the same charge, and thus tend to repel each other, which lends instability to the overall molecule. This may be eliminated by changing the charge (to an opposite charge or a neutral charge) of one or both of the amino acid moieties so that there is no repelling. Therefore, another class of G-CSF analogs includes those G-CSF analogs having been altered to modify instability due to surface interactions, such as electron charge location.

[0045] The present invention relates to methods for designing G-CSF analogs and related compositions and the products of those methods. The end products of the methods may be the G-CSF analogs as defined above or related compositions. For instance, the examples disclosed herein demonstrate (a) the effects of changes in the constituents (i.e., chemical moieties) of the G-CSF molecule on the G-CSF structure and (b) the effects of changes in structure on biological function. Essentially, therefore, an aspect of the present invention is a method for preparing a G-CSF analog

comprising the steps of:

(a) viewing at an amino acid or atomic level information conveying the three dimensional structure of a G-CSF molecule as set forth in Figure 5 wherein the chemical moieties, such as each amino acid residue or each atom of each amino acid residue, of the G-CSF molecule are correlated with said structure;
(b) selecting from said information a site on a G-CSF molecule for alteration;
(c) preparing a G-CSF analog molecule having such alteration; and
(d) optionally, testing such G-CSF analog molecule for a desired characteristic.

[0046] One may use the here provided computer programs for a computer-based method for preparing a G-CSF analog. Another aspect of the present invention is therefore a method for preparing a G-CSF analog according to the method of the preceeding paragraph based on the use of a computer comprising the steps of:

(a) providing computer expression of the three dimensional structure of a G-CSF molecule wherein the chemical moieties, such as each amino acid residue or each atom of each amino acid residue, of the G-CSF molecule are correlated with said structure;
(b) selecting from said computer expression a site on a G-CSF molecule for alteration;
(c) preparing a G-CSF molecule having such alteration; and
(d) optionally, testing such G-CSF molecule for a desired characteristic.

[0047] More specifically, the present invention provides a method for preparing a G-CSF analog comprising the steps of:

(a) viewing at the amino acid or atomic level the three dimensional structure of a G-CSF molecule as set forth in Figure 5 via a computer, said computer programmed (i) to express the coordinates of a G-CSF molecule in three dimensional space, and (ii) to allow for entry of information for alteration of said G-CSF expression and viewing thereof;
(b) selecting a site on said visual image of said G-CSF molecule for alteration;
(c) entering information for said alteration on said computer;
(d) viewing a three dimensional structure of said altered G-CSF molecule via said computer;
(e) optionally repeating steps (a)-(e);
(f) preparing a G-CSF analog with said alteration; and
(g) optionally testing said G-CSF analog for a desired characteristic.

[0048] In another aspect, the present disclosure relates to methods of using the present G-CSF analogs and related compositions and methods for the treatment or protection of mammals, either alone or in combination with other hematopoietic factors or drugs in the treatment of hematopoietic disorders. It is contemplated that one aspect of designing G-CSF analogs will be the goal of enhancing or modifying the characteristics non-modified G-CSF is known to have.
[0049] For example, the analogs may possess enhanced or modified activities, so, where G-CSF is useful in the treatment of (for example) neutropenia, the present compositions and methods may also be of such use.
[0050] Another example is the modification of G-CSF for the purpose of interacting more effectively when used in combination with other factors particularly in the treatment of hematopoietic disorders. One example of such combination use is to use an early-acting hematopoietic factor (i.e., a factor which acts earlier in the hematopoiesis cascade on relatively undifferentiated cells) and either simultaneously or in seriatim use of a later-acting hematopoietic factor, such as G-CSF or analog thereof (as G-CSF acts on the CFU-GM lineage in the selective stimulation of neutrophils). The methods and compositions may be useful in therapy involving such combinations or "cocktails" of hematopoietic factors.
[0051] The compositions and methods may also be useful in the treatment of leukopenia, mylogenous leukemia, severe chronic neutropenia, aplastic anemia, glycogen storage disease, mucosistitis, and other bone marrow failure states. The compositions and methods may also be useful in the treatment of hematopoietic deficits arising from chemotherapy or from radiation therapy. The success of bone marrow transplantation, or the use of peripheral blood progenitor cells for transplantation, for example, may be enhanced by application of the present compositions (proteins or nucleic acids for gene therapy) and methods. The compositions and methods may also be useful in the treatment of infectious diseases, such in the context of wound healing, burn treatment, bacteremia, septicemia, fungal infections, endocarditis, osteopyelitis, infection related to abdominal trauma, infections not responding to antibiotics, pneumonia and the treatment of bacterial inflammation may also benefit from the application of the compositions and methods. In addition, the compositions and methods may be useful in the treatment of leukemia based upon a reported ability to differentiate leukemic cells. Welte et al., PNAS-USA 82: 1526-1530 (1985). Other applications include the treatment of individuals with tumors, using the compositions and methods, optionally in the presence of receptors (such as antibod-

ies) which bind to the tumor cells. For review articles on therapeutic applications, see Lieshhke and Burgess, N.Engl.J.Med. 327: 28-34 and 99-106 (1992) both of which are herein incorporated by reference.

[0052] The compositions and methods may also be useful to act as intermediaries in the production of other moieties; for example, G-CSF has been reported to influence the production of other hematopoietic factors and this function (if ascertained) may be enhanced or modified via the present compositions and/or methods.

[0053] The compositions related to the present G-CSF analogs, such as receptors, may be useful to act as an antagonist which prevents the activity of G-CSF or an analog. One may obtain a composition with some or all of the activity of non-altered G-CSF or a G-CSF analog, and add one or more chemical moieties to alter one or more properties of such G-CSF or analog. With knowledge of the three dimensional conformation, one may forecast the best geographic location for such chemical modification to achieve the desired effect.

[0054] General objectives in chemical modification may include improved half-life (such as reduced renal, immunological or cellular clearance), altered bioactivity (such as altered enzymatic properties, dissociated bioactivities or activity in organic solvents), reduced toxicity (such as concealing toxic epitopes, compartmentalization, and selective biodistribution), altered immunoreactivity (reduced immunogenicity, reduced antigenicity or adjuvant action), or altered physical properties (such as increased solubility, improved thermal stability, improved mechanical stability, or conformational stabilization). See Francis, *Focus on Growth Factors* 3: 4-10 (May 1992) (published by Mediscript, Mountview Court, Friern Barnet Lane, London N20 OLD, UK).

[0055] The examples below are illustrative of the present invention and are not intended as a limitation. It is understood that variations and modifications will occur to those skilled in the art, and it is intended that the appended claims cover all such equivalent variations which come within the scope of the invention as claimed.

Detailed Description of the Drawings

[0056]

FIGURE 1 is an illustration of the amino acid sequence of the 174 amino acid species of G-CSF with an additional N-terminal methionine (Seq. ID No.: 1) (Seq. ID No.: 2).

FIGURE 2 is an topology diagram of the crystalline structure of G-CSF, as well as hGH, pGH, GM-CSF, INF-B, IL-2, and IL-4. These illustrations are based on inspection of cited references. The length of secondary structural elements are drawn in proportion to the number of residues. A, B, C, and D helices are labeled according to the scheme used herein for G-CSF. For INF-β, the original labeling of helices is indicated in parentheses. FIGURE 3 is an "ribbon diagram" of the three dimensional structure of G-CSF. Helix A is amino acid residues 11-39 (numbered according to Figure 1, above), helix B is amino acid residues 72-91, helix C is amino acid residues 100-123, and helix D is amino acid residues 143-173. The relatively short 3^{10} helix is at amino acid residues 45-48, and the alpha helix is at amino acid residues 48-53. Residues 93-95 form almost one turn of a left handed helix.

FIGURE 4 is a "barrel diagram" of the three dimensional structure of G-CSF. Shown in various shades of gray are the overall cylinders and their orientations for the three dimensional structure of G-CSF. The numbers indicate amino acid residue position according to FIGURE 1 above.

FIGURE 5 is a list of the coordinates used to generate a computer-aided visual image of the three-dimensional structure of G-CSF. The coordinates are set forth below. The columns correspond to separate field:

(i) Field 1 (from the left hand side) is the atom,
(ii) Field 2 is the assigned atom number,
(iii) Field 3 is the atom name (according to the periodic table standard nomenclature, with CB being carbon atom Beta, CG is Carbon atom Gamma, etc.);
(iv) Field 4 is the residue type (according to three letter nomenclature for amino acids as found in, e.g., Stryer, Biochemistry, 3d Ed., W.H. Freeman and Company, N.Y. 1988, inside back cover);
(v) Fields 5-7 are the x-axis, y-axis and z-axis positions of the atom;
(vi) Field 8 (often a "1.00") designates occupancy at that position;
(vii) Field 9 designates the B-factor;
(viii) Field 10 designates the molecule designation. Three molecules (designated a, b, and c) of G-CSF crystallized together as a unit. The designation a, b, or c indicates which coordinates are from which molecule. The number after the letter (1, 2, or 3) indicates the assigned amino acid residue position, with molecule A having assigned positions 10-175, molecule B having assigned positions 210-375, and molecule C having assigned positions 410-575. These positions were so designated so that there would be no overlap among the three molecules which crystallized together. (The "W" designation indicates water).

FIGURE 6 is a schematic representation of the strategy involved in refining the crystallization matrix for parameters

involved in crystallization. The crystallization matrix corresponds to the final concentration of the components (salts, buffers and precipitants) of the crystallization solutions in the wells of a 24 well tissue culture plate. These concentrations are produced by pipetting the appropriate volume of stock solutions into the wells of the microtiter plate. To design the matrix, the crystallographer decides on an upper and lower concentration of the component. These upper and lower concentrations can be pipetted along either the rows (e.g., A1-A6, B1-B6, C1-C6 or D1-D6) or along the entire tray (A1-D6). The former method is useful for checking reproducibility of crystal growth of a single component along a limited number of wells, whereas the later method is more useful in initial screening. The results of several stages of refinement of the crystallization matrix are illustrated by a representation of three plates. The increase in shading in the wells indicates a positive crystallization result which, in the final stages, would be X-ray quality crystals but in the initial stages could be oil droplets, granular precipitates or small crystals approximately less than 0.05 mm in size. Part A represents an initial screen of one parameter in which the range of concentration between the first well (A1) and last well (D6) is large and the concentration increase between wells is calculated as ((concentration A1)-(concentration D6))/23). Part B represents that in later stages of the crystallization matrix refinement of the concentration spread between A1 and D6 would be reduced which would result in more crystals formed per plate. Part C indicates a final stage of matrix refinement in which quality crystals are found in most wells of the plate.

Detailed Description of the Invention

[0057] The present invention grows out of the discovery of the three dimensional structure of G-CSF. This three dimensional structure has been expressed via computer program for stereoscopic viewing. By viewing this stereoscopically, structure-function relationships identified and G-CSF analogs have been designed and made.

The Overall Three Dimensional Structure of G-CSF

[0058] The G-CSF used to ascertain the structure was a non-glycosylated 174 amino acid species having an extra N-terminal methionine residue incident to bacterial expression. The DNA and amino acid sequence of this G-CSF are illustrat d in FIGURE 1.

[0059] Overall, the three dimensional structure of G-CSF is predominantly helical, with 103 of the 175 residues forming a 4-alpha-helical bundle. The only other secondary structure is found in the loop between the first two long helices where a 4 residue 3^{10} helix is immediately followed by a 6 residue alpha helix. As shown in FIGURE 2, the overall structure has been compared with the structure reported for other proteins: growth hormone (Abdel-Meguid et al., PNAS-USA 84: 6434 (1987) and Vos et al., Science 255: 305-312 (1992)), granulocyte macrophage colony stimulating factor (Diederichs et al., Science 254: 1779-1782 (1991), interferon-β (Senda et al., EMBO J. 11: 3193-3201 (1992)), interleukin-2 (McKay Science 257: 1673-1677 (1992)) and interleukin-4 (Powers et al., Science 256: 1673-1677 (1992), and Smith et al., J. Mol. Biol. 224: 899-904 (1992)). Structural similarity among these growth factors occurs despite the absence of similarity in their amino acid sequences.

[0060] Presently, the structural information was correlation of G-CSF biochemistry, and this can be summarized as follows (with sequence position 1 being at the N-terminus):

Sequence Position	Description of Structure	Analysis
1-10	Extended chain	Deletion causes no loss of biological activity
Cys 18	Partially buried	Reactive with DTNB and Thimersososl but not with iodo-acetate
34	Alternative splice site	Insertion reduces biological activity
20-47 (inclusive)	Helix A, first disulfide and portion of AB helix	Predicted receptor binding region based on neutralizing antibody data
20, 23, 24	Helix A	Single alanine mutation of residue(s) reduces biological activity. Predicted receptor binding (Site B).
165-175 (inclusive)	Carboxy terminus	Deletion reduces biological activity

[0061] This biochemical information, having been gleaned from antibody binding studies, see Layton et al., Biochemistry 266: 23815-23823 (1991), was superimposed on the three-dimensional structure in order to design G-CSF analogs. The design, preparation, and testing of these G-CSF analogs is described in Example 1 below.

EXAMPLE 1

[0062] This Example describes the preparation of crystalline G-CSF, the visualization of the three dimensional structure of recombinant human G-CSF via computer-generated image, the preparation of analogs, using site-directed mutagenesis or nucleic acid amplification methods, the biological assays and HPLC analysis used to analyze the G-CSF analogs, and the resulting determination of overall structure/function relationships. All cited publications are herein incorporated by reference.

A. Use of Automated Crystallization

[0063] The need for a three-dimensional structure of recombinant human granulocyte colony stimulating factor (r-hu-G-CSF), and the availability of large quantities of the purified protein, led to methods of crystal growth by incomplete factorial sampling and seeding. Starting with the implementation of incomplete factorial crystallization described by Jancarik and Kim, J. Appl. Crystallogr. 24: 409 (1991) solution conditions that yielded oil droplets and birefringence aggregates were ascertained. Also, software and hardware of an automated pipetting system were modified to produce some 400 different crystallization conditions per day. Weber, J. Appl. Crystallogr. 20: 366-373 (1987). This procedure led to a crystallization solution which produced r-hu-G-CSF crystals.

[0064] The size, reproducibility and quality of the crystals was improved by a seeding method in which the number of "nucleation initiating units" was estimated by serial dilution of a seeding solution. These methods yielded reproducible growth of 2.0 mm r-hu-G-CSF crystals. The space group of these crystals is $P2_12_12_1$ with cell dimensions of a=90 Å, b=110 Å and c=49 Å, and they diffract to a resolution of 2.0 Å.

1. Overall Methodology

[0065] To search for the crystallizing conditions of a new protein, Carter and Carter, J. Biol. Chem. 254: 12219-12223 (1979) proposed the incomplete factorial method. They suggested that a sampling of a large number of randomly selected, but generally probable, crystallizing conditions may lead to a successful combination of reagents that produce protein crystallization. This idea was implemented by Jancarik and Kim, J. Appl. Crystallogr. 24: 409(1991), who described 32 solutions for the initial crystallization trials which cover a range of pH, salts and precipitants. Here we describe an extension of their implementation to an expanded set of 70 solutions. To minimize the human effort and error of solution preparation, the method has been programmed for an automatic pipetting machine.

[0066] Following Weber's method of successive automated grid searching (SAGS), J.Cryst. Growth 90: 318-324(1988), the robotic system was used to generate a series of solutions which continually refined the crystallization conditions of temperature, pH, salts and precipitant. Once a solution that could reproducibly grow crystals was determined, a seeding technique which greatly improved the quality of the crystals was developed. When these methods were combined, hundreds of diffraction quality crystals (crystals diffracting to at least about 2.5 Angstroms, preferably having at least portions diffracting to below 2 Angstroms, and more preferably, approximately 1 Angstrom) were produced in a few days.

[0067] Generally, the method for crystallization, which may be used with any protein one desires to crystallize, comprises the steps of:

(a) combining aqueous aliquots of the desired protein with either (i) aliquots of a salt solution, each aliquot having a different concentration of salt; or (ii) aliquots of a precipitant solution, each aliquot having a different concentration of precipitant, optionally wherein each combined aliquot is combined in the presence of a range of pH;
(b) observing said combined aliquots for precrystalline formations, and selecting said salt or precipitant combination and said pH which is efficacious in producing precrystalline forms, or, if no precrystalline forms are so produced, increasing the protein starting concentration of said aqueous aliquots of protein;
(c) after said salt or said precipitant concentration is selected, repeating step (a) with said previously unselected solution in the presence of said selected concentration; and
(d) repeating step (b) and step (a) until a crystal of desired quality is obtained.

[0068] The above method may optionally be automated, which provides vast savings in time and labor. Preferred protein starting concentrations are between 10mg/ml and 20mg/ml, however this starting concentration will vary with the protein (the G-CSF below was analyzed using 33mg/ml). A preferred range of salt solution to begin analysis with is

(NaCl) of 0-2.5M. A preferred precipitant is polyethylene glycol 8000, however, other precipitants include organic solvents (such as ethanol), polyethylene glycol molecules having a molecular weight in the range of 500-20,000, and other precipitants known to those skilled in the art. The preferred pH range is pH 4.5 , 5.0, 5.5, 6.0, 6.5, 7.0, 7.5, 8.0, 8.5, and 9.0. Precrystallization forms include oils, birefringement precipitants, small crystals (< approximately 0.05 mm), medium crystals (approximately 0.5 to .5 mm) and large crystals (> approximately 0.5 mm). The preferred time for waiting to see a crystalline structure is 48 hours, although weekly observation is also preferred, and generally, after about one month, a different protein concentration is utilized (generally the protein concentration is increased). Automation is preferred, using the Accuflex system as modified. The preferred automation parameters are described below.

[0069] Generally, protein with a concentration between 10 mg/ml and 20 mg/ml was combined with a range of NaCl solutions from 0-2.5 M, and each such combination was performed (separately) in the presence of the above range of concentrations. Once a precrystallization structure is observed, that salt concentration and pH range are optimized in a separate experiment, until the desired crystal quality is achieved. Next, the precipitant concentration, in the presence of varying levels of pH is also optimized. When both are optimized, the optimal conditions are performed at once to achieve the desired result (this is diagrammed in FIGURE 6).

a. Implementation of an automated pipetting system

[0070] Drops and reservoir solutions were prepared by an Accuflex pipetting system (ICN Pharmaceuticals, Costa Mesa, CA) which is controlled by a personal computer that sends ASCII codes through a standard serial interface. The pipetter samples six different solutions by means of a rotating valve and pipettes these solutions onto a plate whose translation in a x-y coordinate system can be controlled. The vertical component of the system manipulates a syringe that is capable both of dispensing and retrieving liquid.

[0071] The software provided with the Accuflex was based on the SAGS method as proposed by Cox and Weber, J.Appl. Crystallogr. 20: 366-373 (1987). This method involves the systematic variation of two major crystallization parameters, pH and precipitant concentration, with provision to vary two others. While building on these concepts, the software used here provided greater flexibility in the design and implementation of the crystallization solutions used in the automated grid searching strategy. As a result of this flexibility the present software also created a larger number of different solutions. This is essential for the implementation of the incomplete factorial method as described in that section below.

[0072] To improve the speed and design of the automated grid searching strategy, the Accuflex pipetting system required software and hardware modifications. The hardware changes allowed the use of two different micro-titer trays, one used for handing drop and one used for sitting drop experiments, and a Plexiglas tray which held 24 additional buffer, salt and precipitant solutions. These additional solutions expanded the grid of crystallizing conditions that could be surveyed.

[0073] To utilize the hardware modifications, the pipetting software was written in two subroutines; one subroutine allows the crystallographer to design a matrix of crystallization solutions based on the concentrations of their components and the second subroutine to translate these concentrations into the computer code which pipettes the proper volumes of the solutions into the crystallization trays. The concentration matrices can be generated by either of two programs. The first program (MRF, available from Amgen, Inc., Thousand Oaks, CA) refers to a list of stock solution concentrations supplied by the crystallographer and calculates the required volume to be pipette to achieve the designated concentration. The second method, which is preferred, incorporates a spread sheet program (Lotus) which can be used to make more sophisticated gradients of precipitants or pH. The concentration matrix created by either program is interpreted by the control program (SUX, a modification of the program found in the Accuflex pipetter originally and available from Amgen, Inc., Thousand Oaks, CA) and the wells are filled accordingly.

b. Implementation of the Incomplete Factorial Method

[0074] The convenience of the modified pipetting system for preparing diverse solutions improved the implementation of an expanded incomplete factorial method. The development of a new set of crystallization solutions having "random" components was generated using the program INFAC, Carter et al., J.Cryst. Growth 90: 60-73(1988) which produced a list containing 96 random combinations of one factor from three variables. Combinations of calcium and phosphate which immediately precipitated were eliminated, leaving 70 distinct combinations of precipitants, salts and buffers. These combinations were prepared using the automated pipetter and incubated for 1 week. The mixtures were inspected and solutions which formed precipitants were prepared again with lower concentrations of their components. This was repeated until all wells were clear of precipitant.

c. Crystallization of r-hu-G-CSF

[0075] Several different crystallization strategies were used to find a solution which produced x-ray quality crystals. These strategies included the use of the incomplete factorial method, refinement of the crystallization conditions using successive automated grid searches (SAGS), implementation of a seeding technique and development of a crystal production procedure which yielded hundreds of quality crystals overnight. Unless otherwise noted the screening and production of r-hu-G-CSF crystals utilized the hanging drop vapor diffusion method. Afinsen et al., Physical principles of protein crystallization. In: Eisenberg (ed.), Advances in Protein Chemistry 41: 1-33 (1991).

[0076] The initial screening for crystallization conditions of r-hu-G-CSF used the Jancarik and Kim, J.Appl.Crystallogr. 24: 409(1991) incomplete factorial method which resulted in several solutions that produced "precrystallization" results. These results included birefringent precipitants, oils and very small crystals (< .05 mm). These precrystallizations solutions then served as the starting points for systematic screening.

[0077] The screening process required the development of crystallization matrices. These matrices corresponded to the concentration of the components in the crystallization solutions and were created using the IBM-PC based spread sheet Lotus™ and implemented with the modified Accuflex pipetting system. The strategy in designing the matrices was to vary one crystallization condition (such as salt concentration) while holding the other conditions such as pH, and precipitant concentration constant. At the start of screening, the concentration range of the varied condition was large but the concentration was successively refined until all wells in the micro-titer tray produced the same crystallization result. These results were scored as follows: crystals, birefringement precipitate, granular precipitate, oil droplets and amorphous mass. If the concentration of a crystallization parameter did not produce at least a precipitant, the concentration of that parameter was increased until a precipitant formed. After each tray was produced, it was left undisturbed for at least two days and then inspected for crystal growth. After this initial screening, the trays were then inspected on a weekly basis.

[0078] From this screening process, two independent solutions with the same pH and precipitant but differing in salts (MgCl, $LiSO_4$) were identified which produced small (0.1 x 0.05 x 0.05 mm) crystals. Based on these results, a new series of concentration matrices were produced which varied MgCl with respect to $LiSO_4$ while keeping the other crystallization parameters constant. This series of experiments resulted in identification of a solution which produced diffraction quality crystals (> approximately 0.5 mm) in about three weeks. To find this crystallization growth solution (100 mM Mes pH 5.8, 380 mM $MgCl_2$, 220 mM LiSO4 and 8% PEG 8k) approximately 8,000 conditions had been screened which consumed about 300 mg of protein.

[0079] The size of the crystals depended on the number of crystals forming per drop. Typically 3 to 5 crystals would be formed with average size of (1.0 x 0.7 x 0.7 mm). Two morphologies which had an identical space group ($P2_12_12_1$) and unit cell dimensions a=90.2, b=110.2, c=49.5 were obtained depending on whether or not seeding (see below) was implemented. Without seeding, the r-hu-G-CSF crystals had one long flat surface and rounded edges.

[0080] When seeding was employed, crystals with sharp faces were observed in the drop within 4 to 6 hours (0.05 by 0.05 by 0.05 mm). Within 24 hours, crystals had grown to (0.7 by 0.7 by 0.7 mm) and continued to grow beyond 2 mm depending on the number of crystals forming in the drop.

d. Seeding and determination of nucleation initiation sites.

[0081] The presently provided method for seeding crystals establishes the number of nucleation initiation units in each individual well used (here, after the optimum conditions for growing crystals had been determined). The method here is advantageous in that the number of "seeds" affects the quality of the crystals, and this in turn affects the degree of resolution. The present seeding here also provides advantages in that with seeding, G-CSF crystal grows in a period of about 3 days, whereas without seeding, the growth takes approximately three weeks.

[0082] In one series of production growth (see methods), showers of small but well defined crystals were produced overnight (<0.01 x 0.01 x0.01 mm). Crystallization conditions were followed as described above except that a pipette tip employed in previously had been reused. Presumably, the crystal showering effect was caused by small nucleation units which had formed in the used tip and which provided sites of nucleation for the crystals. Addition of a small amount (0.5 ul) of the drops containing the crystal showers to a new drop under standard production growth conditions resulted in a shower of crystals overnight. This method was used to produce several trays of drops containing crystal showers which we termed "seed stock".

[0083] The number of nucleation initiation units (NIU) contained within the "seed stock" drops was estimated to attempt to improve the reproducibility and quality of the r-hu-GCSF crystals. To determine the number of NIU in the "seed stock", an aliquot of the drop was serially diluted along a 96 well microtiter plate. The microtiter plate was prepared by adding 50 ul of a solution containing equal volumes of r-hu-G-CSF (33 mg/ml) and the crystal growth solution (described above) in each well. An aliquot (3 ul) of one of the "seed stock" drops was transferred to the first well of the microtiter plate. The solution in the well was mixed and 3 ul was then transferred to the next well along the row of the

microtiter plate. Each row of the microtiter plate was similarly prepared and the tray was sealed with plastic tape. Overnight, small crystals formed in the bottom of the wells of the microtiter plate and the number of crystals in the wells were correlated to the dilution of the original "seed stock". To produce large single crystals, the "seed stock" drop was appropriately diluted into fresh CGS and then an aliquot of this solution containing the NIU was transferred to a drop

[0084] Once crystallization conditions had been optimized, crystals were grown in a production method in which 3 ml each of CGS and r-hu-G-CSF (33 mg/ml) were mixed to create 5 trays (each having 24 wells). This method included the production of the refined crystallization solution in liter quantities, mixing this solution with protein and placing the protein/crystallization solution in either hanging drop or sitting drop trays. This process typically yielded 100 to 300 quality crystals (>0.5 mm) in about 5 days.

e. Experimental Methods

Materials

[0085] Crystallographic information was obtained starting with r-hu-met-G-CSF with the amino acid sequence as provided in FIGURE 1 with a specific activity of 1.0 +/- 0.6 x 10^8U/mg (as measured by cell mitogenesis assay in a 10 mM acetate buffer at pH 4.0 (in Water for Injection) at a concentration of approximately 3 mg/ml solution was concentrated with an Amicon concentrator at 75 psi using a YM10 filter. The solution was typically concentrated 10 fold at 4°C and stored for several months.

Initial Screening

[0086] Crystals suitable for X-ray analysis were obtained by vapor-diffusion equilibrium using hanging drops. For preliminary screening, 7 ul of the protein solution at 33 mg/ml (as prepared above) was mixed with an equal volume of the well solution, placed on siliconized glass plates and suspended over the well solution utilizing Linbro tissue culture plates (Flow Laboratories, McLean, Va). All of the pipetting was performed with the Accuflex pipetter, however, trays were removed from the automated pipetter after the well solutions had been created and thoroughly mixed for at least 10 minutes with a table top shaker. The Linbro trays were then returned to the pipetter which added the well and protein solutions to the siliconized cover slips. The cover slips were then inverted and sealed over 1 ml of the well solutions with silicon grease.

[0087] The components of the automated crystallization system are as follows. A PC-DOS computer system was used to design a matrix of crystallization solutions based on the concentration of their components. These matrices were produced with either MRF of the Lotus spread sheet (described above). The final product of these programs is a data file. This file contains the information required by the SUX program to pipette the appropriate volume of the stock solutions to obtain the concentrations described in the matrices. The SUX program information was passed through a serial I/O port and used to dictate to the Accuflex pipetting system the position of the valve relative to the stock solutions, the amount of solution to be retrieved, and then pipetted into the wells of the microtiter plates and the X-Y position of each well (the column/row of each well). Addition information was transmitted to the pipetter which included the Z position (height) of the syringe during filling as well as the position of a drain where the system pauses to purge the syringe between fillings of different solutions. The 24 well microtiter plate (either Linbro or Cryschem) and cover slip holder was placed on a plate which was moved in the X-Y plane. Movement of the plate allowed the pipetter to position the syringe to pipette into the wells. It also positioned the coverslips and vials and extract solutions from these sources. Prior the pipetting, the Linbro microtiter plates had a thin film of grease applied around the edges of the wells. After the crystallization solutions were prepared in the wells and before they were transferred to the cover slips, the microtiter plate was removed from the pipetting system, and solutions were allowed to mix on a table top shaker for ten minutes. After mixing, the well solution was either transferred to the cover slips (in the case of the hanging drop protocol) or transferred to the middle post in the well (in the case of the sitting drop protocol). Protein was extracted from a vial and added to the coverslip drop containing the well solution (or to the post). Plastic tape was applied to the top of the Cryschem plate to seal the wells.

Production Growth

[0088] Once conditions for crystallization had been optimized, crystal growth was performed utilizing a "production" method. The crystallization solution which contained 100 mM Mes pH 5.8, 380 mM MgCl2, 220 mM LiSO4, and 8% PEG 8K was made in 1 liter quantities. Utilizing an Eppindorf syringe pipetter, 1 ml aliquots of this solution were pipetted into each of the wells of the Linbro plate. A solution containing 50% of this solution and 50% G-CSF (33 mg/ml) was mixed and pipetted onto the siliconized cover slips. Typical volumes of these drops were between 50 and 100 ul and because of the large size of these drops, great care was taken in flipping the coverslips and suspending the drops over

the wells.

Data Collection

[0089] The structure has been refined with X-PLOR (Bruniger, X-PLOR version 3.0, A system for crystallography and NMR, Yale University, New Haven CT) against 2.2Å data collected on an R-AXIS (Molecular Structure, Corp. Houston, TX) imaging plate detector.

f. Observations

[0090] As an effective recombinant human therapeutic, r-hu-G-CSF has been produced in large quantities and gram levels have been made available for structural analysis. The crystallization methods provided herein are likely to find other applications as other proteins of interest become available. This method can be applied to any crystallographic project which has large quantities of protein (approximately >200 mg). As one skilled in the art will recognize, the present materials and methods may be modified and equivalent materials and methods may be available for crystallization of other proteins.

B. Computer Program For Visualizing The Three Dimensional Structure of G-CSF

[0091] Although diagrams, such as those in the Figures herein, are useful for visualizing the three dimensional structure of G-CSF, a computer program which allows for stereoscopic viewing of the molecule is contemplated as preferred. This stereoscopic viewing, or "virtual reality" as those in the art sometimes refer to it, allows one to visualize the structure in its three dimensional form from every angle in a wide range of resolution, from macromolecular structure down to the atomic level. The computer programs contemplated herein also allow one to change perspective of the viewing angle of the molecule, for example by rotating the molecule. The contemplated programs also respond to changes so that one may, for example, delete, add, or substitute one or more images of atoms, including entire amino acid residues, or add chemical moieties to existing or substituted groups, and visualize the change in structure.

[0092] Other computer based systems may be used; the elements being: (a) a means for entering information, such as orthogonal coordinates or other numerically assigned coordinates of the three dimensional structure of G-CSF; (b) a means for expressing such coordinates, such as visual means so that one may view the three dimensional structure and correlate such three dimensional structure with the composition of the G-CSF molecule, such as the amino acid composition; (c) optionally, means for entering information which alters the composition of the G-CSF molecule expressed, so that the image of such three dimensional structure displays the altered composition.

[0093] The coordinates for the preferred computer program used are presented in FIGURE 5. The preferred computer program is Insight II, version 4, available from Biosym in San Diego, CA. For the raw crystallographic structure, the observed intensities of the diffraction data ("F-obs") and the orthogonal coordinates are also deposited in the Protein Data Bank, Chemistry Department, Brookhaven National Laboratory, Upton, New York 19723, USA and these are herein incorporated by reference.

[0094] Once the coordinates are entered into the Insight II program, one can easily display the three dimensional G-CSF molecule representation on a computer screen. The preferred computer system for display is Silicon Graphics 320 VGX (San Diego, CA). For stereoscopic viewing, one may wear eyewear (Crystal Eyes, Silicon Graphics) which allows one to visualize the G-CSF molecule in three dimensions stereoscopically, so one may turn the molecule and envision molecular design.

[0095] Thus, the present invention provides a method of designing or preparing a G-CSF analog with the aid of a computer comprising:

(a) providing said computer with the means for displaying the three dimensional structure of a G-CSF molecule including displaying the composition of moieties of said G-CSF molecule, preferably displaying the three dimensional location of each amino acid, and more preferably displaying the three dimensional location of each atom of a G-CSF molecule;
(b) viewing said display;
(c) selecting a site on said display for alteration in the composition of said molecule or the location of a moiety; and
(d) preparing a G-CSF analog with such alteration.

[0096] The alteration may be selected based on the desired structural characteristics of the end-product G-CSF analog, and considerations for such design are described in more detail below. Such considerations include the location and compositions of hydrophobic amino acid residues, particularly residues internal to the helical structures of a G-CSF molecule which residues, when altered, alter the overall structure of the internal core of the molecule and may prevent

receptor binding; the location and compositions of external loop structures, alteration of which may not affect the overall structure of the G-CSF molecule.

[0097] FIGURES 2-4 illustrate the overall three dimensional conformation in different ways. The topological diagram, the ribbon diagram, and the barrel diagram all illustrate aspects of the conformation of G-CSF.

[0098] FIGURE 2 illustrates a comparison between G-CSF and other molecules. There is a similarity of architecture, although these growth factors differ in the local conformations of their loops and bundle geometrics. The up-up-down-down topology with two long crossover connections is conserved, however, among all six of these molecules, despite the dissimilarity in amino acid sequence.

[0099] FIGURE 3 illustrates in more detail the secondary structure of recombinant human G-CSF. This ribbon diagram illustrates the handedness of the helices and their positions relative to each other.

[0100] FIGURE 4 illustrates in a different way the conformation of recombinant human G-CSF. This "barrel" diagram illustrates the overall architecture of recombinant human G-CSF.

C. Preparation of Analogs Using M13 Mutagenesis

[0101] This example relates to the preparation of G-CSF analogs using site directed mutagenesis techniques involving the single stranded bacteriophage M13, according to methods published in PCT Application No. WO 85/00817 (Souza et al., published February 28, 1985, herein incorporated by reference). This method essentially involves using a single-stranded nucleic acid template of the non-mutagenized sequence, and binding to it a smaller oligonucleotide containing the desired change in the sequence. Hybridization conditions allow for non-identical sequences to hybridize and the remaining sequence is filled in to be identical to the original template. What results is a double stranded molecule, with one of the two strands containing the desired change. This mutagenized single strand is separated, and used itself as a template for its complementary strand. This creates a double stranded molecule with the desired change.

[0102] The original G-CSF nucleic acid sequence used is presented in FIGURE 1, and the oligonucleotides containing the mutagenized nucleic acid(s) are presented in Table 2. Abbreviations used herein for amino acid residues and nucleotides are conventional, see Stryer, Biochemistry, 3d Ed., W.H. Freeman and Company, N.Y., N.Y. 1988, inside back cover.

[0103] The original G-CSF nucleic acid sequence was first placed into vector M13mp21. The DNA from single stranded phage M13mp21 containing the original G-CSF sequence was then isolated, and resuspended in water. For each reaction, 200 ng of this DNA was mixed with a 1.5 pmole of phosphorylated oligonucleotide (Table 2) and suspend d in 0.1M Tris, 0.01M $MgCl_2$, 0.005M DTT, 0.1mM ATP, pH 8.0. The DNAs were annealed by heating to 65°C and slowly cooling to room temperature.

[0104] Once cooled, 0.5mM of each ATP, dATP, dCTP, dGTP, TTP, 1 unit of T4 DNA ligase and 1 unit of Klenow fragment of E. coli polymerase 1 were added to the 1 unit of annealed DNA in 0.1M Tris, 0.025M NaCl, 0.01M $MgCl_2$, 0.01M DTT, pH 7.5.

[0105] The now double stranded, closed circular DNA was used to transfect E. coli without further purification. Plaques were screened by lifting the plaques with nitrocellulose filters, and then hybridizing the filters with single stranded DNA end-labeled with P^{32} for 1 hour at 55-60°C. After hybridization, the filters were washed at 0-3°C below the melt temperature of the oligo (2°C for A-T, 4°C for G-C) which selectively left autoradiography signals corresponding to plaques with phage containing the mutated sequence. Positive clones were confirmed by sequencing.

[0106] Set forth below are the oligonucleotides used for each G-CSF analog prepared via the M13 mutagenesis method. The nomenclature indicates the residue and the position of the original amino acid (e.g., Lysine at position 17), and the residue and position of the substituted amino acid (e.g., arginine 17). A substitution involving more than one residue is indicated via superscript notation, with commas between the noted positions or a semicolon indicating different residues. Deletions with no substitutions are so noted. The oligonucleotide sequences used for M13-based mutagenesis are next indicated; these oligonucleotides were manufactured synthetically, although the method of preparation is not critical, any nucleic acid synthesis method and/or equipment may be used. The length of the oligo is also indicated. As indicated above, these oligos were allowed to contact the single stranded phage vector, and then single nucleotides were added to complete the G-CSF analog nucleic acid sequence.

Table 2

G-CSF ANALOGS	SEQUENCES (5'-> 3')	Length (nucleotide)	Seq. ID
Lys^{17}->Arg^{17}	CTT TCT GCT GCG TTG TCT GGA ACA	24	3
Lys^{24}->Arg^{24}	ACA GGT TCG TCG TAT CCA GGG TG	23	4
Lys^{35}->Arg^{35}	CAC TGC AAG AAC GTC TGT GCG CT	23	5
Lys^{41}->Arg^{41}	CGC TAC TTA CCG TCT GTG CCA TC	23	6
$Lys^{17,24,35}$-> $Arg^{17,24,35}$	CTT TCT GCT GCG TTG TCT GGA ACA	24	7
	ACA GGT TCG TCG TAT CCA GGG TG	23	8
	CAC TGC AAG AAC GTC TGT GCG CT	23	9
$Lys^{17,24,41}$-> $Arg^{17,24,41}$	CTT TCT GCT GCG TTG TCT GGA ACA	24	10
	ACA GGT TCG TCG TAT CCA GGG TG	23	11
	CGC TAC TTA CCG TCT GTC CCA TC	23	12
$Lys^{17,35,41}$-> $Arg^{17,35,41}$	CTT TCT GCT GCG TTG TCT GGA ACA	24	13
	CAC TGC AAG AAC GTC TGT GCG CT	23	14
	CGC TAC TTA CCG TCT GTG CCA TC	23	15
$Lys^{24,35,41}$-> $Arg^{24,35,41}$	ACA GGT TCG TCG TAT CCA GGG TG	23	16
	CAC TGC AAG AAC GTC TGT GCG CT	23	17
	CGC TAC TTA CCG TCT GTG CCA TC	23	18

Table 2 (con't)

G-CSF ANALOGS	SEQUENCES (5'-> 3')	Length (nucleotide)	Seq. ID
$Lys^{17,24,35,41}$-> $Arg^{17,24,35,41}$	CTT TCT GCT GCG TTG TCT GGA ACA	24	19
	ACA GGT TCG TCG TAT CCA GGG TG	23	20
	CAC TGC AAG AAC GTC TGT GCG CT	23	21
	CGC TAC TTA CCG TCT GTG CCA TC	23	22
Cys^{18}->Ala^{18}	TCT GCT GAA AGC TCT GGA ACA GG	23	23
Gln^{68}->Glu^{68}	CTT GTC CAT CTG AAG CTC TTC AG	23	24
$Cys^{37,43}$-> $Ser^{37,43}$	GAA AAA CTG TCC GCT ACT TAC AAA CTG TCC CAT CCG G	37	25
Gln^{26}->Ala^{26}	TTC GTA AAA TCG CGG GTG ACG G	22	26
Gln^{174}->Ala^{174}	TCA TCT GGC TGC GCC GTA ATA G	22	27
Arg^{170}->Ala^{170}	CCG TGT TCT GGC TCA TCT GGC T	22	28
Arg^{167}->Ala^{167}	GAA GTA TCT TAC GCT GTT CTG CGT	24	29
Deletion 167	GAA GTA TCT TAC TAA GTT CTG CGT C	25	30
Lys^{41}->Ala^{41}	CGC TAC TTA CGC ACT GTG CCA T	22	31
His^{44}->Lys^{44}	CAA ACT GTG CAA GCC GGA AGA G	22	32
Glu^{47}->Ala^{47}	CAT CCG GAA GCA CTG GTA CTG C	22	33

Table 2 (con't)

G-CSF ANALOGS	SEQUENCES (5'-> 3')	Length (nucleotide)	Seq. ID
Arg^{23}->Ala^{23}	GGA ACA GGT TGC TAA AAT CCA GG	23	34
Lys^{24}->Ala^{24}	GAA CAG GTT CGT GCG ATC CAG GGT G	25	35
Glu^{20}->Ala^{20}	GAA ATG TCT GGC ACA GGT TCG T	22	36
Asp^{28}->Ala^{28}	TCC AGG GTG CCG GTG CTG C	19	37
Met^{127}->Glu^{127}	AAG AGC TCG GTG AGG CAC CAG CT	23	38
Met^{138}->Glu^{138}	CTC AAG GTG CTG AGC CGG CAT TC	23	39
Met^{127}->Leu^{127}	GAG CTC GGT CTG GCA CCA GC	20	40
Met^{138}->Leu^{138}	TCA AGG TGC TCT GCC GGC ATT	21	41
Ser^{13}->Ala^{13}	TCT GCC GCA AGC CTT TCT GCT GA	23	42
Lys^{17}->Ala^{17}	CTT TCT GCT GGC ATG TCT GGA ACA	24	43
Gln^{121}->Ala^{121}	CTA TTT GGC AAG CGA TGG AAG AGC	24	44
Glu^{124}->Ala^{124}	CAG ATG GAA GCG CTC GGT ATG	21	45

Table 2 (con't)

G-CSF ANALOGS	SEQUENCES (5'-> 3')	Length (nucleotide)	Seq. ID
$Met^{127,138}$-> $Leu^{127,138}$	GAG CTC GGT CTG GCA CCA GC	20	46
	TCA AGG TGC TCT GCC GGC ATT	21	47
**Glu^{20}->Ala^{20}; Ser^{13}->Gly^{13}	GAA ATG TCT GGC ACA GGT TCG T	22	48

** This analog came about during the preparation of G-CSF analog Glu^{20}->Ala^{20}. As several clones were being sequenced to identify the Glu^{20}->Ala^{20} analog, the Glu^{20}->Ala^{20}; Ser^{13}->Gly^{13} analog was identified. This double mutant was the result of an *in vitro* Klenow DNA polymerase reaction mistake.

D. Preparation of G-CSF Analogs Using DNA Amplification

[0107] This example relates to methods for producing G-CSF analogs using a DNA amplification technique. Essentially, DNA encoding each analog was amplified in two separate pieces, combined, and then the total sequence itself amplified. Depending upon where the desired change in the original G-CSF DNA was to be made, internal primers were used to incorporate the change, and generate the two separate amplified pieces. For example, for amplification of the 5' end of the desired analog DNA, a 5' flanking primer (complementary to a sequence of the plasmid upstream from the G-CSF original DNA) was used at one end of the region to be amplified, and an internal primer, capable of hybridizing to the original DNA but incorporating the desired change, was used for priming the other end. The resulting amplified region stretched from the 5' flanking primer through the internal primer. The same was done for the 3' terminus, using a 3' flanking primer (complementary to a sequence of the plasmid downstream from the G-CSF original DNA) and an internal primer complementary to the region of the intended mutation. Once the two "halves" (which may or may not be equal in size, depending on the location of the internal primer) were amplified, the two "halves" were allowed to connect. Once connected, the 5' flanking primer and the 3' flanking primer were used to amplify the entire sequence containing the desired change.

[0108] If more than one change is desired, the above process may be modified to incorporate the change into the internal primer, or the process may be repeated using a different internal primer. Alternatively, the gene amplification process may be used with other methods for creating changes in nucleic acid sequence, such as the phage based mutagenesis technique as described above. Examples of process for preparing analogs with more than one change are described below.

[0109] To create the G-CSF analogs described below, the template DNA used was the sequence as in FIGURE 1 plus certain flanking regions (from a plasmid containing the G-CSF coding region). These flanking regions were used as the 5' and 3' flanking primers and are set forth below. The amplification reactions were performed in 40 ul volumes containing 10 mM Tris-HCl, 1.5 mM $MgCl_2$, 50 mM KCl, 0.1 mg/ml gelatin, pH 8.3 at 20°C. The 40 ul reactions also contained 0.1mM of each dNTP, 10 pmoles of each primer, and 1 ng of template DNA. Each amplification was repeated for 15 cycles. Each cycle consisted of 0.5 minutes at 94°C, 0.5 minutes at 50°C, and 0.75 minutes at 72°C. Flanking primers were 20 nucleotides in length and internal primers were 20 to 25 nucleotides in length. This resulted in multiple copies of double stranded DNA encoding either the front portion or the back portion of the desired G-CSF analog.

[0110] For combining the two "halves," one fortieth of each of the two reactions was combined in a third DNA amplification reaction. The two portions were allowed to anneal at the internal primer location, as their ends bearing the mutation were complementary, and following a cycle of polymerization, give rise to a full length DNA sequence. Once so annealed, the whole analog was amplified using the 5' and 3' flanking primers. This amplification process was repeated for 15 cycles as described above.

[0111] The completed, amplified analog DNA sequence was cleaved with XbaI and XhoI restriction endonuclease to produce cohesive ends for insertion into a vector. The cleaved DNA was placed into a plasmid vector, and that vector was used to transform E. coli. Transformants were challenged with kanamycin at 50 ug/ml and incubated at 30°C. Production of G-CSF analog protein was confirmed by polyacrylamide gel electrophoresis of a whole cell lysate. The presence of the desired mutation was confirmed by DNA sequence analysis of plasmid purified from the production isolate. Cultures were then grown, and cells were harvested, and the G-CSF analogs were purified as set forth below.

[0112] Set forth below in Table 3 are the specific primers used for each analog made using gene amplification.

Table 3

Analog Seq. ID	Internal Primer(5'->3')	
His^{44}->Ala^{44}	5'primer-TTCCGGAGCGCACAGTTTG	49
	3'primer-CAAACTGTGGGCTCCGGAAGAGC	50
Thr^{117}->Ala^{117}	5'primer-ATGCCAAATTGCAGTAGCAAAG	51
	3'primer-CTTTGCTACTGCAATTTGGCAACA	52
Asp^{110}->Ala^{110}	5'primer-ATCAGCTACTGCTAGCTGCAGA	53
	3'primer-TCTGCAGCTAGCAGTAGCTGACT	54
Gln^{21}->Ala^{21}	5'primer-TTACGAACCGCTTCCAGACATT	55
	3'primer-AATGTCTGGAAGCGGTTCGTAAAAT	56

Table 3 (continued)

Analog Seq. ID	Internal Primer(5'->3')	
Asp^{113}->Ala^{113}	5'primer-GTAGCAAATGCAGCTACATCTA	57
	3'primer-TAGATGTAGCTGCATTTGCTACTAC	58
His^{53}->Ala^{53}	5'primer-CCAAGAGAAGCACCCAGCAG	59
	3'primer-CTGCTGGGTGCTTCTCTTGGGA	60
For each analog, the following 5' flanking primer was used:		
	5'-CACTGGCGGTGATAATGAGC	61
For each analog, the following 3' flanking primer was used:		
	3'-GGTCATTACGGACCGGATC	62

1. Consfruction of Double Mutation

[0113] To make G-CSF analog $Gln^{12,21}$->$Glu^{12,21}$, two separate DNA amplifications were conducted to create the two DNA mutations. The template DNA used was the sequence as in FIGURE 1 plus certain flanking regions (from a plasmid containing the G-CSF coding region). The precise sequences are listed below. Each of the two DNA amplification reactions were carried out using a Perkin Elmer/Cetus DNA Thermal Cycler. The 40 ul reaction mix consisted of 1X PCR Buffer (Cetus), 0.2 mM each of the 4 dXTPs (Cetus), 50 pmoles of each primer oligonucleotide, 2 ng of G-CSF template DNA (on a plasmid vector), and 1 unit of Taq polymerase (Cetus). The amplification process was carried out for 30 cycles. Each cycle consisted of 1minute at 94°C, 2 minutes at 50°C, and 3 minutes at 72°C.

[0114] DNA amplification "A" used the oligonucleotides:
5' CCACTGGCGGTGATACTGAGC 3' (Seq. ID 63) and
5' AGCAGAAAGCTTTCCGGCAGAGAAGAAGCAGGA 3' (Seq. ID 64)

[0115] DNA amplification "B" used the oligonucleotides:
5' GCCGCAAAGCTTTCTGCTGAAATGTCTGGAAGAGGTTCGTAAAATCCAGGGTGA 3' (Seq. ID 65) and
5' CTGGAATGCAGAAGCAAATGCCGGCATAGCACCTTCAGTCGGTTGCAGAGCTGGTGCCA 3' (Seq. ID 66)

[0116] From the 109 base pair double stranded DNA product obtained after DNA amplification "A", a 64 base pair XbaI to HindIII DNA fragment was cut and isolated that contained the DNA mutation Gln^{12}->Glu^{12}. From the 509 base pair double stranded DNA product obtained after DNA amplification "B", a 197 base pair HindIII to BsmI DNA fragment was cut and isolated that contained the DNA mutation Gln^{21}->Glu^{21}.

[0117] The "A" and "B" fragments were ligated together with a 4.8 kilo-base pair XbaI to BsmI DNA plasmid vector fragment. The ligation mix consisted of equal molar DNA restriction fragments, ligation buffer (25 mM Tris-HCl pH 7.8, 10 mM $MgCl_2$, 2 mM DTT, 0.5 mM rATP, and 100 ug/ml BSA) and T4 DNA ligase and was incubated overnight at 14°C. The ligated DNA was then transformed into E. coli FM5 cells by electroporation using a Bio Rad Gene Pulsar apparatus (BioRad, Richmond, CA). A clone was isolated and the plasmid construct verified to contain the two mutations by DNA sequencing. This 'intermediate' vector also contained a deletion of a 193 base pair BsmI to BsmI DNA fragment. The final plasmid vector was constructed by ligation and transformation (as described above) of DNA fragments obtained by cutting and isolating a 2 kilo-base pair SstI to BamHI DNA fragment from the intermediate vector, a 2.8 kbp SstI to EcoRI DNA fragment from the plasmid vector, and a 360 bp BamHI to EcoRI DNA fragment from the plasmid vector. The final construct was verified by DNA sequencing the G-CSF gene. Cultures were grown, and the cells were harvested, and the G-CSF analogs were purified as set forth below.

[0118] As indicated above, any combination of mutagenesis techniques may be used to generate a G-CSF analog nucleic acid (and expression product) having one or more than one alteration. The two examples above, using M13-based mutagenesis and gene amplification-based mutagenesis, are illustrative.

E. Expression of G-CSF Analog DNA

[0119] The G-CSF analog DNAs were then placed into a plasmid vector and used to transform E. coli strain FM5 (ATCC#53911). The present G-CSF analog DNAs contained on plasmids and in bacterial host cells are available from the American Type Culture Collection, Rockville, MD, and the accession designations are indicated below.

[0120] One liter cultures were grown in broth containing 10g tryptone, 5g yeast extract and 5g NaCl) at 30°C until reaching a density at A^{600} of 0.5, at which point they were rapidly heated to 42°C. The flasks were allowed to continue shaking at for three hours.

[0121] Other prokaryotic or eukaryotic host cells may also be used, such as other bacterial cells, strains or species, mammalian cells in culture (COS, CHO or other types) insect cells or multicellular organs or organisms, or plant cells or multicellular organs or organisms, and a skilled practitioner will recognize the appropriate host. The present G-CSF analogs and related compositions may also be prepared synthetically, as, for example, by solid phase peptide synthesis methds, or other chemical manufacturing techniques. Other cloning and expression systems will be apparent to those skilled in the art.

F. Purification of G-CSF Analog Protein

[0122] Cells were harvested by centrifugation (10,000 x G, 20 minutes, 4°C). The pellet (usually 5 grams) was resuspended in 30 ml of 1mM DTT and passed three times through a French press cell at 10,000 psi. The broken cell suspension was centrifuged at 10,000g for 30 minutes, the supernatant removed, and the pellet resuspended in 30-40 ml water. This was recentrifuged at 10,000 x G for 30 minutes, and this pellet was dissolved in 25 ml of 2% Sarkosyl and 50mM Tris at pH 8. Copper sulfate was added to a concentration of 40uM, and the mixture was allowed to stir for at least 15 hours at 15-25°C. The mixture was then centrifuged at 20,000 x G for 30 minutes. The resultant solubilized protein mixture was diluted four-fold with 13.3 mM Tris, pH 7.7, the Sarkosyl was removed, and the supernatant was then applied to a DEAE-cellulose (Whatman DE-52) column equilibrated in 20mM Tris, pH 7.7. After loading and washing the column with the same buffer, the analogs were eluted with 20mM Tris /NaCl (between 35mM to 100mM depending on the analog, as indicated below), pH 7.7. For most of the analogs, the eluent from the DEAE column was adjusted to a pH of 5.4, with 50% acetic acid and diluted as necessary (to obtain the proper conductivity) with 5mM sodium acetate pH 5.4. The solution was then loaded onto a CM-sepharose column equilibrated in 20 mM sodium acetate, pH 5.4. The column was then washed with 20mM NaAc, pH 5.4 until the absorbance at 280 nm was approximately zero. The G-CSF analog was then eluted with sodium acetate/NaCl in concentrations as described below in Table 4. The DEAE column eluents for those analogs not applied to the CM-sepharose column were dialyzed directly into 10mM NaAc, ph 4.0 buffer. The purified G-CSF analogs were then suitably isolated for in vitro analysis. The salt concentrations used for eluting the analogs varied, as noted above. Below, the salt concentrations for the DEAE cellulose column and for the CM-sepharose column are listed:

Table 4

Salt Concentrations

Analog	DEAE Cellulose	CM-Sepharose
Lys^{17}->Arg^{17}	35mM	37.5mM
Lys^{24}->Arg^{24}	35mM	37.5mM
Lys^{35}->Arg^{35}	35mM	37.5mM
Lys^{41}->Arg^{41}	35mM	37.5mM
$Lys^{17,24,35}$->$Arg^{17,24,35}$	35mM	37.5mM
$Lys^{17,35,41}$->$Arg^{17,35,41}$	35mM	37.5mM

Table 4 Con't

Analog	DEAE Cellulose	CM-Sepharose
$Lys^{24,35,41}$->$Arg^{24,35,41}$	35mM	37.5mM
$Lys^{17,24,35,41}$->$Arg^{17,24,35,41}$	35mM	37.5mM
$Lys^{17,24,41}$->$Arg^{17,24,41}$	35mM	37.5mM
Gln^{68}->Glu^{68}	60mM	37.5mM
$Cys^{37,43}$->$Ser^{37,43}$	40mM	37.5mM
Gln^{26}->Ala^{26}	40mM	40mM
Gln^{174}->Ala^{174}	40mM	40mM
Arg^{170}->Ala^{170}	40mM	40mM
Arg^{167}->Ala^{167}	40mM	40mM
Deletion 167*	N/A	N/A
Lys^{41}->Ala^{41}	160mM	40mM
His^{44}->Lys^{44}	40mM	60mM
Glu^{47}->Ala^{47}	40mM	40mM
Arg^{23}->Ala^{23}	40mM	40mM
Lys^{24}->Ala^{24}	120mM	40mM
Glu^{20}->Ala^{20}	40mM	60mM
Asp^{28}->Ala^{28}	40mM	80mM
Met^{127}->Glu^{127}	80mM	40mM
Met^{138}->Glu^{138}	80mM	40mM
Met^{127}->Leu^{127}	40mM	40mM
Met^{138}->Leu^{138}	40mM	40mM
Cys^{18}->Ala^{18}	40mM	37.5mM
$Gln^{12,21}$->$Glu^{12,21}$	60mM	37.5mM
$Gln^{12,21,68}$->$Glu^{12,21,68}$ Glu^{20}->Ala^{20}; Ser^{13}->Gly^{13}	60mM 40mM	37.5mM 80mM

Table 4 Con't

Analog	DEAE Cellulose	CM-Sepharose
$Met^{127,138}$->$Leu^{127,138}$	40mM	40mM
Ser^{13}->Ala^{13}	40mM	40mM
Lys^{17}->Ala^{17}	80mM	40mM
Gln^{121}->Ala^{121}	40mM	60mM
Gln^{21}->Ala^{21}	50mM	Gradient 0 -150mM
His^{44}->Ala^{44}**	40mM	N/A
His^{53}->Ala^{53}**	50mM	N/A
Asp^{110}->Ala^{110}**	40mM	N/A
Asp^{113}->Ala^{113}**	40mM	N/A
Thr^{117}->Ala^{117}**	50mM	N/A
Asp^{28}->Ala^{28}; Asp^{110} Ala^{110}**	50mM	N/A
Glu^{124}->Ala^{124}**	40mM	40mM

* For Deletion ^{167}, the data are unavailable.
** For these analogs, the DEAE cellulose column alone was use for purification.

[0123] The above purification methods are illustrative, and a skilled practitioner will recognize that other means are available for obtaining the present G-CSF analogs.

G. Biological Assays

[0124] Regardless of which methods were used to create the present G-CSF analogs, the analogs were subject to assays for biological activity. Tritiated thymidine assays were conducted to ascertain the degree of cell division. Other biological assays, however, may be used to ascertain the desired activity. Biological assays such as assaying for the ability to induce terminal differentiation in mouse WEHI-3B (D+) leukemic cell line, also provides indication of G-CSF activity. See Nicola, et al., Blood 54: 614-27 (1979). Other in vitro assays may be used to ascertain biological activity. See Nicola, Annu. Rev. Biochem. 58: 45-77 (1989). In general, the test for biological activity should provide analysis for the desired result, such as increase or decrease in biological activity (as compared to non-altered G-CSF), different biological activity (as compared to non-altered G-CSF), receptor affinity analysis, or serum half-life analysis. The list is incomplete, and those skilled in the art will recognize other assays useful for testing for the desired end result.

[0125] The ^{3}H-thymidine assay was performed using standard methods. Bone marrow was obtained from sacrificed female Balb C mice. Bone marrow cells were briefly suspended, centrifuged, and resuspended in a growth medium. A 160 ul aliquot containing approximately 10,000 cells was placed into each well of a 96 well micro-titer plate. Samples of the purified G-CSF analog(as prepared above) were added to each well, and incubated for 68 hours. Tritiated thymidine was added to the wells and allowed to incubate for 5 additional hours. After the 5 hour incubation time, the cells were harvested, filtered, and thoroughly rinsed. The filters were added to a vial containing scintillation fluid. The beta emissions were counted (LKB Betaplate scintillation counter). Standards and analogs were analyzed in triplicate, and samples which fell substantially above or below the standard curve were re-assayed with the proper dilution.

The results reported here are the average of the triplicate analog data relative to the unaltered recombinant human G-CSF standard results.

H. HPLC Analysis

[0126] High pressure liquid chromatography was performed on purified samples of analog. Alth ugh peak position on a reverse phase HPLC column is not a definitive indication of structural similarity between two proteins, analogs which have similar retention times may have the same type of hydrophobic interactions with the HPLC column as the non-altered molecule. This is one indication of an overall similar structure.

[0127] Samples of the analog and the non-altered recombinant human G-CSF were analyzed on a reverse phase (0.46 x 25 cm) Vydac 214TP54 column (Separations Group, Inc. Hesperia, CA). The purified analog G-CSF samples were prepared in 20 mM acetate and 40 mM NaCl solution buffered at pH 5.2 to a final concentration of 0.1 mg/ml to 5 mg/ml, depending on how the analog performed in the column. Varying amounts (depending on the concentration) were loaded onto the HPLC column, which had been equilibrated with an aqueous solution containing 1% isopropanol, 52.8% acetonitrile, and .38% trifluoro acetate (TFA). The samples were subjected to a gradient of 0.86%/minute acetonitrile, and .002% TFA.

I. Results

[0128] Presented below are the results of the above biological assays and HPLC analysis. Biological activity is the average of triplicate data and reported as a percentage of the control standard (non-altered G-CSF). Relative HPLC peak position is the position of the analog G-CSF relative to the control standard (non-altered G-CSF) peak. The "+" or "-" symbols indicate whether the analog HPLC peak was in advance of or followed the control standard peak (in minutes). Not all of the variants had been analyzed for relative HPLC peak, and only those so analyzed are included below. Also presented are the American Type Culture Collection designations for E. coli host cells containing the nucleic acids coding for the present analogs, as prepared above.

Table 5

Seq. ID	Variant	Analog	Relative HPLC Peak	ATCC No.	% Normal G-CSF Activity
67	1	Lys^{17}->Arg^{17}	N/A	69184	N/A
68	2	Lys^{24}->Arg^{24}	N/A	69185	N/A
69	3	Lys^{35}->Arg^{35}	N/A	69186	N/A
70	4	Lys^{41}->Arg^{41}	N/A	69187	N/A
71	5	$Lys^{17,24,35}$->$Arg^{17,24,35}$	N/A	69189	N/A
72	6	$Lys^{17,35,41}$->$Arg^{17,35,41}$	N/A	69192	N/A
73	7	$Lys^{24,35,41}$->$Arg^{24,35,41}$	N/A	69191	N/A
74	8	$Lys^{17,24,35,41}$ ->$Arg^{17,24,35,41}$	N/A	69193	N/A
75	9	$Lys^{17,24,41}$->$Arg^{17,24,41}$	N/A	69190	N/A
76	10	Gln^{68}->Glu^{68}	N/A	69196	N/A
77	11	$Cys^{37,43}$->$Ser^{37,43}$	N/A	69197	N/A
78	12	Gln^{26}->Ala^{26}	+.96	69201	51%
79	13	Gln^{174}->Ala^{174}	+.14	69202	100%
80	14	Arg^{170}->Ala^{170}	+.78	69203	100%

Table 5 Con't

Seq. ID	Variant	Analog	Relative HPLC Peak	ATCC No.	% Normal G-CSF Activity
81	15	Arg^{167}->Ala^{167}	+.54	69204	110%
82	16	Deletion 167	-.99	69207	N/A
83	17	Lys^{41}->Ala^{41}	+.25	69208	81%
84	18	His^{44}->Lys^{44}	-1.53	69212	70%
85	19	Glu^{47}->Ala^{47}	+.14	69205	0%
86	20	Arg^{23}->Ala^{23}	-.03	69206	31%
87	21	Lys^{24}->Ala^{24}	+1.95	69213	0%
88	22	Glu^{20}->Ala^{20}	-0.07	69211	0%
89	23	Asp^{28}->Ala^{28}	-.30	69210	147%
90	24	Met^{127}->Glu^{127}	N/A	69223	N/A
91	25	Met^{138}->Glu^{138}	N/A	69222	N/A
92	26	Met^{127}->Leu^{127}	N/A	69198	N/A
93	27	Met^{138}->Leu^{138}	N/A	69199	N/A
94	28	Cys^{18}->Ala^{18}	N/A	69188	N/A
95	29	$Gln^{12,21}$->$Glu^{12,21}$	N/A	69194	N/A
96	30	$Gln^{12,21,68}$->$Glu^{12,21,68}$	N/A	69195	N/A
97	31	Glu^{20}->Ala^{20}; Ser^{13}	+1.74	69209	0%

Table 5 Con't

Seq. ID	Variant	Analog	Relative HPLC Peak	ATCC No.	% Normal G-CSF Activity
		->Gly^{13}			
98	32	$Met^{127,138}$->$Leu^{127,138}$	+1.43	69200	98%
99	33	Ser^{13}->Ala^{13}	0	69221	110%
100	34	Lys^{17}->Ala^{17}	+.50	69226	70%
101	35	Gln^{121}->Ala^{121}	+2.7	69225	100%
102	36	Gln^{21}->Ala^{21}	+0.63	69217	9.6%
103	37	His^{44}->Ala^{44}	+1.52	69215	10.8%
104	38	His^{53}->Ala^{53}	+0.99	69219	8.3%
105	39	Asp^{110}->Ala^{110}	+1.97	69216	29%
106	40	Asp^{113}->Ala^{113}	-0.34	69218	0%
107	41	Thr^{117}->Ala^{117}	+0.4	69214	9.7%
108	42	Asp^{28}->Ala^{28}; Asp^{110} Ala^{110}	+3.2	69220	20.6%

Table 5 Con't

Seq. ID	Variant	Analog	Relative HPLC Peak	ATCC No.	% Normal G-CSF Activity
109	43	Glu^{124}->Ala^{124}	+0.16	69224	75%
110	44	Phe^{114}->Val^{114}, T^{117}->A^{117}**	+0.53		0%

**This analog was apparently a result of an inadvertent error in the oligo which was used to prepare number 41, above (Thr^{117}->Ala^{117}), and thus was prepared identically to the process used for that analog.

"N/A" indicates data which are not available.

1. Identification of Structure-Function Relationships

[0129] The first step used to design the present analogs was to determine what moieties are necessary for structural integrity of the G-CSF molecule. This was done at the amino acid residue level, although the atomic level is also available for analysis. Modification of the residues necessary for structural integrity results in change in the overall structure of the G-CSF molecule. This may or may not be desirable, depending on the analog one wishes to produce. The working examples here were designed to maintain the overall structural integrity of the G-CSF molecule, for the purpose of maintain G-CSF receptor binding of the analog to the G-CSF receptor (as used in this section below, the "G-CSF receptor" refers to the natural G-CSF receptor, found on hematopoietic cells). It was assumed, and confirmed by the studies presented here, that G-CSF receptor binding is a necessary step for at least one biological activity, as determined by the above biological assays.

[0130] As can be seen from the figures, G-CSF (here, recombinant human met-G-CSF) is an antiparallel 4-alpha helical bundle with a left-handed twist, and with overall dimensions of 45 Å x 30Å x 24Å. The four helices within the bundle are referred to as helices A, B, C and D, and their connecting loops are known as the AB, BC and CD loops. The helix crossing angles range from -167.5° to -159.4°. Helices A, B, and C are straight, whereas helix D contains two kinds of structural characteristics, at Gly 150 and Ser 160 (of the recombinant human met-G-CSF). Overall, the G-CSF molecules is a bundle of four helices, connected in series by external loops. This structural information was then correlated with known functional information. It was known that residues (including methionine at position 1) 47, 23, 24, 20, 21, 44, 53, 113, 110, 28 and 114 may be modified, and the effect on biological activity would be substantial.

[0131] The majority of single mutations which lowered biological activity were centered around two regions of G-CSF that are separated by 30Å, and are located on different faces of the four helix bundle. One region involves interactions between the A helix and the D helix. This is further confirmed by the presence of salt bridges in the non-altered molecule as follows:

Atom	Helix	Atom	Helix	Distance
Arg 170 N1	D	Tyr 166 OH	A	3.3
Tyr 166 OH	D	Arg 23 N2	A	3.3
Glu 163 OE1	D	Arg 23 N1	A	2.8
Arg 23 N1	A	Gln 26 OE1	A	3.1
Gln 159 NE2	D	Gln 26 O	A	3.3

[0132] Distances reported here were for molecule A, as indicated in FIGURE 5 (wherein three G-CSF molecules crystallized together and were designated as A, B, and C). As can be seen, there is a web of salt bridges between helix A and helix D, which act to stabilize the helix A structure, and therefore affect the overall structure of the G-CSF molecule.

[0133] The area centering around residues Glu 20, Arg 23 and Lys 24 are found on the hydrophilic face of the A helix (residues 20-37). Substitution of the residues with the non-charged alanine residue at positions 20 and 23 resulted in similar HPLC retention times, indicating similarity in structure. Alteration of these sites altered the biological activity (as indicated by the present assays). Substitution at Lys 24 altered biological activity, but did not result in a similar HPLC retention time as the other two alterations.

[0134] The second site at which alteration lowered biological activity involves the AB helix. Changing glutamine at position 47 to alanine (analog no. 19, above) reduced biological activity (in the thymidine uptake assay) to zero. The AB helix is predominantly hydrophobic, except at the amino and carboxy termini; it contains one turn of a 3^{10} helix. There are two histadines at each termini (His 44 and His 56) and an additional glutamate at residue 46 which has the potential to form a salt bridge to His 44. The fourier transformed infra red spectrographic analysis (FTIR) of the analog suggests this analog is structurally similar to the non-altered recombinant G-CSF molecule. Further testing showed that this analog would not crystallize under the same conditions as the non-altered recombinant molecule.

[0135] Alterations at the carboxy terminus (Gln 174, Arg 167 and Arg 170) had little effect on biological activity. In contrast, deletion of th- last eight residues (167-175) lowered biological activity. These results may indicat- that the deletion destabilizes the overall structure which prevents the mutant from proper binding to the G-CSF receptor (and thus initiating signal transduction).

[0136] Generally, for the G-CSF internal core -- the internal four helix bundle lacking the external loops --the hydrophobic internal residues are essential for structural integrity. For example, in helix A, the internal hydrophobic residues

are (with methionine being position 1) Phe 14, Cys 18, Val 22, Ile 25, Ile 32 and Leu 36. Generally, for the G-CSF internal core -- the internal four helix bundle lacking the external loops --the hydrophobic internal residues are essential for structural integrity. For example, in helix A, the internal hydrophobic residues are (with methionine being position 1 as in FIGURE 1) Phe 14, Cys 18, Val 22, Ile 25, Ile 32 and Leu 36. The other hydrophobic residues (again with the met at position 1) are: helix B, Ala 72, Leu 76, Leu 79, Leu 83, Tyr 86, Leu 90 Leu 93; helix C, Leu 104, Leu 107, Val 111, Ala 114, Ile 118, Met 122; and helix D, Val 154, Val 158, Phe 161, Val 164, Val 168, Leu 172.

[0137] The above biological activity data, from the presently prepared G-CSF analogs, demonstrate that modification of the external loops interfere least with G-CSF overall structure. Preferred loops for analog prepration are the AB loop and the CD loop. The loops are relatively flexible structures as compared to the helices. The loops may contribute to the proteolysis of the molecule. G-CSF is relatively fast acting in vivo as the purpose the molecule serves is to generate a response to a biological challenge, i.e., selectively stimulate neutrophils. The G-CSF turnover rate is also relatively fast. The flexibility of the loops may provide a "handle" for proteases to attach to the molecule to inactivate the molecule. Modification of the loops to prevent protease degradation, yet have (via retention of the overall structure of non-modified G-CSF) no loss in biological activity may be accomplished.

[0138] This phenomenon is probably not limited to the G-CSF molecule but may also be common to the other molecules with known similar overall structures, as presented in Figure 2. Alteration of the external loop of, for example hGH, Interferon B, IL-2, GM-CSF and IL-4 may provide the least change to the overall structure. The external loops on the GM-CSF molecule are not as flexible as those found on the G-CSF molecule, and this may indicate a longer serum life, consistent with the broader biological activity of GM-CSF. Thus, the external loops of GM-CSF may be modified by releasing the external loops from the beta-sheet structure, which may make the loops more flexible (similar to those G-CSF) and therefore make the molecule more susceptible to protease degradation (and thus increase the turnover rate).

[0139] Alteration of these external loops may be effected by stabilizing the loops by connection to one or more of the internal helices. Connecting means are known to those in the art, such as the formation of a beta sheet, salt bridge, disulfide bonding or hydrophobic interactions, and other means are available. Also, deletion of one or more moieties, such as one or more amino acid residues or portions thereof, to prepare an abbreviated molecule and thus eliminate certain portions of the external loops may be effected.

[0140] Thus, by alteration of the external loops, preferably the AB loop (amino acids 58-72 of r-hu-met G-CSF) or the CD loop (amino acids 119 to 145 of r-hu-met-G-CSF), and less preferably the amino terminus (amino acids 1-10), one may therefore modify the biological function without elimination of G-CSF receptor binding. For example, one may: (1) increase half-life (or prepare an oral dosage form, for example) of the G-CSF molecule by, for example, decreasing the ability of proteases to act on the G-CSF molecule or adding chemical modifications to the G-CSF molecule, such as one or more polyethylene glycol molecules or enteric coatings for oral formulation which would act to change some characteristic of the G-CSF molecule as described above, such as increasing serum or other half-life or decreasing antigenicity; (2) prepare a hybrid molecule, such as combining G-CSF with part or all of another protein such as another cytokine or another protein which effects signal transduction via entry through the cell through a G-CSF receptor transport mechanism; or (3) increase the biological activity as in, for example, the ability to selectively stimulate neutrophils (as compared to a non-modified G-CSF molecule). This list is not limited to the above exemplars.

[0141] Another aspect observed from the above data is that stabilizing surface interactions may affect biological activity. This is apparent from comparing analogs 23 and 40. Analog 23 contains a substitution of the charged asparagine residue at position 28 for the neutrally-charged alanine residue in that position, and such substitution resulted in a 50% increase in the biological activity (as measured by the disclosed thymidine uptake assays). The asparagine residue at position 28 has a surface interaction with the asparagine residue at position 113; both residues being negatively charged, there is a certain amount of instability (due to the repelling of like charged moieties). When, however the asparagine at position 113 is replaced with the neutrally-charged alanine, the biological activity drops to zero (in the present assay system). This indicates that the asparagine at position 113 is critical to biological activity, and elimination of the asparagine at position 28 serves to increase the effect that asparagine at position 113 possesses.

[0142] The domains required for G-CSF receptor binding were also determined based on the above analogs prepared and the G-CSF structure. The G-CSF receptor binding domain is located at residues (with methionine being position 1) 11-57 (between the A and AB helix) and 100-118 (between the B and C helices). One may also prepare abbreviated molecules capable of binding to a G-CSF receptor and initiate signal transduction for selectively stimulating neutrophils by changing the external loop structure and having the receptor binding domains remain intact.

[0143] Residues essential for biological activity and presumably G-CSF receptor binding or signal transduction have been identified. Two distinct sites are located on two different regions of the secondary structure. What is here called "Site A" is located on a helix which is constrained by salt bridge contacts betw en two other members of the helical bundle. The second site, "Site B" is located on a relatively more flexible helix, AB. The AB helix is potentially more sensitive to local pH changes because of the type and position of the residues at the carboxy and amino termini. Th functional importance of this flexible helix may be important in a conformationally induced fit when binding to the G-CSF receptor. Additionally, the extended portion of the D helix is also indicated to be a G-CSF receptor binding domain, as

ascertained by direct mutational and indirect comparative protein structure analysis. Deletion of the carboxy terminal end of r-hu-met-G-CSF reduces activity as it does for hGH, see, Cunningham and Wells, Science 244: 1081-1084 (1989). Cytokines which have similar structures, such as IL-6 and GM-CSF with predicted similar topology also center their biological activity along the carboxy end of the D helix, see Bazan, Immunology Today 11: 350-354 (1990)

[0144] A comparison of the structures and the positions of G-CSF receptor binding determinants between G-CSF and hGH suggests both molecules have similar means of signal transduction. Two separate G-CSF receptor binding sites have been identified for hGH De Vos et al., Science 255: 306-32 (1991). One of these binding sites (called "Site I") is formed by residues on the exposed faces of hGH's helix 1, the connection region between helix 1 and 2, and helix 4. The second binding site (called "Site II") is formed by surface residues of helix 1 and helix 3.

[0145] The G-CSF receptor binding determinates identified for G-CSF are located in the same relative positions as those identified for hGH. The G-CSF receptor binding site located in the connecting region between helix A and B on the AB helix (Site A) is similar in position to that reported for a small piece of helix (residues 38-47) of hGH. A single point mutation in the AB helix of G-CSF significantly reduces biological activity (as ascertained in the present assays), indicating the role in a G-CSF receptor-ligand interface. Binding of the G-CSF receptor may destabilize the 3^{10} helical nature of this region and induce a conformation change improving the binding energy of the ligand/G-CSF receptor complex.

[0146] In the hGH receptor complex, the first helix of the bundle donates residues to both of the binding sites required to dimerize the hGH receptor Mutational analysis of the corresponding helix of G-CSF (helix A) has identified three residues which are required for biological activity. Of these three residues, Glu 20 and Arg 24 lie on one face of the helical bundle towards helix C, whereas the side chain of Arg 23 (in two of the three molecules in the asymmetric unit) points to the face of the bundle towards helix D. The position of side chains of these biologically important residues indicates that similar to hGH, G-CSF may have a second G-CSF receptor binding site along the interface between helix A and helix C. In contrast with the hGH molecule, the amino terminus of G-CSF has a limited biological role as deletion of the first 11 residues has little effect on the biological activity.

[0147] As indicated above (see FIGURE 2, for example), G-CSF has a topological similarity with other cytokines. A correlation of the structure with previous biochemical studies, mutational analysis and direct comparison of specific residues of the hGH receptor complex indicates that G-CSF has two receptor binding sites. Site A lies along the interface of the A and D helices and includes residues in the small AB helix. Site B also includes residues in the A helix but lies along the interface between helices A and C. The conservation of structure and relative positions of biologically important residues between G-CSF and hGH is one indication of a common method of signal transduction in that the receptor is bound in two places. It is therefore found that G-CSF analogs possessing altered G-CSF receptor binding domains may be prepared by alteration at either of the G-CSF receptor binding sites (residues 20-57 and 145-175).

[0148] Knowledge of the three dimensional structure and correlation of the composition of G-CSF protein makes possible a systematic, rational method for preparing G-CSF analogs. The above working examples have demonstrated that the limitations of the size and polarity of the side chains within the core of the structure dictate how much change the molecule can tolerate before the overall structure is changed.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Amgen Inc.

(ii) TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS

(iii) NUMBER OF SEQUENCES: 110

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Amgen Inc.
(B) STREET: Amgen Center, 1840 DeHavilland Drive
(C) CITY: Thousand Oaks
(D) STATE: California
(E) COUNTRY: United States of America
(F) ZIP: 91320-1789

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 565 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 30..554

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TCTAGAAAAA ACCAAGGAGG TAATAAATA ATG ACT CCA TTA GGT CCT GCT TCT        53
                                    Met Thr Pro Leu Gly Pro Ala Ser
                                      1               5

TCT CTG CCG CAA AGC TTT CTG CTG AAA TGT CTG GAA CAG GTT CGT AAA       101
Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu Gln Val Arg Lys
     10                  15                  20

ATC CAG GGT GAC GGT GCT GCA CTG CAA GAA AAA CTG TGC GCT ACT TAC       149
Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr Tyr
 25                  30                  35                  40
```

```
AAA CTG TGC CAT CCG GAA GAG CTG GTA CTG CTG GGT CAT TCT CTT GGG        197
Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly
                45                  50                  55

ATC CCG TGG GCT CCG CTG TCT TCT TGT CCA TCT CAA GCT CTT CAG CTG        245
Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu
            60                  65                  70

GCT GGT TGT CTG TCT CAA CTG CAT TCT GGT CTG TTC CTG TAT CAG GGT        293
Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly
        75                  80                  85

CTT CTG CAA GCT CTG GAA GGT ATC TCT CCG GAA CTG GGT CCG ACT CTG        341
Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu
    90                  95                  100

GAC ACT CTG CAG CTA GAT GTA GCT GAC TTT GCT ACT ACT ATT TGG CAA        389
Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala Thr Thr Ile Trp Gln
105                 110                 115                 120

CAG ATG GAA GAG CTC GGT ATG GCA CCA GCT CTG CAA CCG ACT CAA GGT        437
Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro Thr Gln Gly
                125                 130                 135

GCT ATG CCG GCA TTC GCT TCT GCA TTC CAG CGT CGT GCA GGA GGT GTA        485
Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
            140                 145                 150

CTG GTT GCT TCT CAT CTG CAA TCT TTC CTG GAA GTA TCT TAC CGT GTT        533
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val
        155                 160                 165

CTG CGT CAT CTG GCT CAG CCG TAATAGAATT C                               565
Leu Arg His Leu Ala Gln Pro
    170                 175
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
  1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45
```

```
Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
 50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
 65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                 85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATTCTGCTG CGTTGTCTGG AACA 24

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACAGGTTCGT CGTATCCAGG GTG 23

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CACTGCAAGA ACGTCTGTGC GCT 23

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGCTACTTAC CGTCTGTGCC ATC 23

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTTTCTGCTG CGTTGTCTGG AACA 24

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACAGGTTCGT CGTATCCAGG GTG 23

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTCTGCAAGA ACGTCTGTGC GCT 23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CTTTCTGCTG CGTTGTCTGG AACA 24

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACAGGTTCGT CGTATCCAGG GTG 23

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGCTACTTAC CGTCTGTCCC ATC 23

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTTTCTGCTG CGTTGTCTGG AACA 24

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTGCAAGA ACGTCTGTGC GCT 23

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CGCTACTTAC CGTCTGTGCC ATC 23

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACAGGTTCGT CGTATCCAGG GTG 23

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CACTGCAAGA ACGTCTGTGC GCT 23

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGCTACTTAC CGTCTGTGCC ATC 23

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTTTCTGCTG CGTTGTCTGG AACA 24

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGGTTCGT CGTATCCAGG GTG 23

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CACTGCAAGA ACGTCTGTGC GCT 23

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGCTACTTAC CGTCTGTGCC ATC 23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TCTGCTGAAA GCTCTGGAAC AGG 23

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTTGTCCATC TGAAGCTCTT CAG 23

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

[illegible]AAACTGT CCGCTACTTA CAAACTGTCC CATCCGG 37

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTCGTAAAAT CGCGGGTGAC GG 22

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCATCTGGCT GCGCCGTAAT AG 22

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCGTGTTCTG GCTCATCTGG CT 22

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAAGTATCTT ACGCTGTTCT GCGT 24

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAAGTATCTT ACTAAGTTCT GCGTC 25

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTACTTAC GCACTGTGCC AT 22

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAAACTGTGC AAGCCGGAAG AG 22

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CATCCGGAAG CACTGGTACT GC 22

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGAACAGGTT GCTAAAATCC AGG 23

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GAACAGGTTC GTGCGATCCA GGGTG 25

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAATGTCTG GCACAGGTTC GT 22

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TCCAGGGTGC CGGTGCTGC 19

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AAGAGCTCGG TGAGGCACCA GCT 23

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTCAAGGTGC TGAGCCGGCA TTC 23

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAGCTCGGTC TGGCACCAGC 20

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

TCAAGGTGCT CTGCCGGCAT T 21

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TGCCGCAA GCCTTTCTGC TGA 23

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTTCTGCTG GCATGTCTGG AACA 24

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CTATTTGGCA AGCGATGGAA GAGC 24

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CAGATGGAAG CGCTCGGTAT G 21

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GAGCTCGGTC TGGCACCAGC 20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

[illegible]AAGGTGCT CTGCCGGCAT T 21

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GAAATGTCTG GCACAGGTTC GT 22

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TTCCGGAGCG CACAGTTTG 19

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGAGAAGGCC TCGGGTGTCA AAC 23

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

ATGCCAAATT GCAGTAGCAA AG 22

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACAACGGTTT AACGTCATCG TTTC 24

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TTCAGCTACT GCTAGCTGCA GA 22

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TCAGTCGATG ACGATCGACG TCT 23

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTACGAACCG CTTCCAGACA TT 22

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TAAAATGCTT GGCGAAGGTC TGTAA 25

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GTAGCAAATG CAGCTACATC TA 22

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CTTCATCGTT TACGTCGATG TAGAT 25

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CCAAGAGAAG CACCCAGCAG 20

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

AGGGTTCTCT TCGTGGGTCG TC 22

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

CACTGGCGGT GATAATGAGC 20

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTAGGCCAGG CATTACTGG 19

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CCACTGGCGG TGATACTGAG C 21

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

AGCAGAAAGC TTTCCGGCAG AGAAGAAGCA GGA 33

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GCCGCAAAGC TTTCTGCTGA AATGTCTGGA AGAGGTTCGT AAAATCCAGG GTGA 54

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CTGGAATGCA GAAGCAAATG CCGGCATAGC ACCTTCAGTC GGTTGCAGAG CTGGTGCCA 59

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Arg Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Arg Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30
```

```
Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
          35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
     50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
 65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                 85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Arg Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95
```

```
Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
                100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
  1                 5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
             20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Arg Leu Cys His Pro Glu Glu Leu
         35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
     50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
 65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                 85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160
```

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
165 170 175

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
1 5 10 15

Arg Cys Leu Glu Gln Val Arg Arg Ile Gln Gly Asp Gly Ala Ala Leu
20 25 30

Gln Glu Arg Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
35 40 45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
50 55 60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65 70 75 80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
85 90 95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
100 105 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
115 120 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
130 135 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145 150 155 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
165 170 175

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Arg Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Arg Leu Cys Ala Thr Tyr Arg Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Arg Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Arg Leu Cys Ala Thr Tyr Arg Leu Cys His Pro Glu Glu Leu
        35                  40                  45
```

```
Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
 50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
 65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                 85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Ile Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1                  5                  10                  15

Arg Cys Leu Glu Gln Val Arg Arg Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Arg Leu Cys Ala Thr Tyr Arg Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
           100                 105                 110
```

```
Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
  1               5                  10                  15

Arg Cys Leu Glu Gln Val Arg Arg Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Arg Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15
Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Glu Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Ile Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Ser Ala Thr Tyr Lys Leu Ser His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

. r Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Ala Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60
```

```
Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
 65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                 85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Ile Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Xaa Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
 65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                 85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125
```

```
Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Ala Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Ala His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Ala Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Val Leu Arg His Leu Ala Gln Pro
                165                 170             174
```

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Ala Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60
```

```
Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
 65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                 85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

...e Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
  1               5                  10                  15

... s Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys Lys Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
 65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                 85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125
```

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
130 135 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145 150 155 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
165 170 175

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
1 5 10 15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
20 25 30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Ala Leu
35 40 45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
50 55 60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65 70 75 80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
85 90 95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
100 105 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
115 120 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
130 135 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145 150 155 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
165 170 175

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Ala Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Ala Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Ala Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60
```

```
Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
 65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Leu Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Leu Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Ala Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125
```

```
Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
  1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Glu Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Glu Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Leu Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Leu Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60
```

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65 70 75 80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
85 90 95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
100 105 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
115 120 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Leu Pro Ala Phe Ala Ser Ala
130 135 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145 150 155 160

Ile Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
165 170 175

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
1 5 10 15

Val Ser Ala Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
20 25 30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
35 40 45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
50 55 60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65 70 75 80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
85 90 95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
100 105 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
115 120 125

```
Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Glu Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Glu Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Glu Ser Phe Leu Leu
1 5 10 15

Lys Cys Leu Glu Glu Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
20 25 30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
35 40 45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
50 55 60

Cys Pro Ser Glu Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65 70 75 80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
85 90 95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
100 105 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
115 120 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
130 135 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145 150 155 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
165 170 175

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Gly Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Ala Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45
```

```
Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
     50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
 65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                 85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Leu Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Leu Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ala Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110
```

```
Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Ala Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Ala Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Ala Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys Ala Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60
```

```
Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
 65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly L u Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

...e Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

...s Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly Ala Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125
```

```
Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
  1                 5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Ala Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
1 5 10 15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
20 25 30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
35 40 45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
50 55 60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65 70 75 80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
85 90 95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
100 105 110

Ala Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
115 120 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
130 135 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145 150 155 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
165 170 175

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

..r Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Phe Ala Thr Ala Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Ala Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60
```

```
Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
 65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                 85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Ala Val Ala
            100                 105                 110

Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
 1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110
```

```
Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Ala Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

```
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu
  1               5                  10                  15

Lys Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu
            20                  25                  30

Gln Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu
        35                  40                  45

Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser
    50                  55                  60

Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His
65                  70                  75                  80

Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
                85                  90                  95

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala
            100                 105                 110

Asp Val Ala Thr Ala Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala
        115                 120                 125

Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala
    130                 135                 140

Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser
145                 150                 155                 160

Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro
                165                 170                 175
```

Claims

1. A method for preparing a G-CSF analog comprising the steps of:

   (a) viewing at the amino acid or atomic level information conveying the three dimensional structure of a G-CSF molecule as set forth in Figure 5;
   (b) selecting from said viewed information at least one site on said G-CSF molecule for alteration;
   (c) preparing a G-CSF molecule having such alteration; and
   (d) optionally, testing such G-CSF molecule for a desired characteristic.

2. A method for preparing a G-CSF analog according to claim 1 based on the use of a computer comprising the steps of:

   (a) providing computer expression at the amino acid or atomic level of the three dimensional structure of a G-CSF molecule as set forth in Figure 5;
   (b) selecting from said computer expression at least one site on said G-CSF molecule for alteration;
   (c) preparing a G-CSF molecule having such alteration; and,
   (d) optionally, testing such G-CSF molecule for a desired characteristic.

3. A method for preparing a G-CSF analog according to claim 2 comprising:

   (a) providing said computer with the means for displaying the three dimensional structure of a G-CSF molecule as set forth in Figure 5; including displaying the composition of moieties of said G-CSF molecule, preferably displaying the three dimensional location of each amino acid, and more preferably displaying the three dimensional location of each atom of a G-CSF molecule;
   (b) viewing said display;
   (c) selecting a site on said display for alteration in the composition of said molecule or the location of a moiety; and
   (d) preparing a G-CSF analog with such alteration.

4. A computer-based method for preparing a G-CSF analog comprising the steps of:

   (a) viewing at the amino acid or atomic level the three dimensional structure of a G-CSF molecule as set forth in Figure 5; via a computer, said computer having been previously programmed (i) to express the coordinates of a G-CSF molecule in three dimensional space, and (ii) to allow for entry of information for alteration of said G-CSF expression and viewing thereof;
   (b) selecting a site on said visual image of said G-CSF molecule for alteration;
   (c) entering information for said alteration on said computer;
   (d) viewing a three dimensional structure of said altered G-CSF molecule via said computer;
   (e) optionally repeating steps (a)-(e) above;
   (f) preparing a G-CSF analog with said alteration; and
   (g) optionally testing said G-CSF analog for a desired characteristic.

Patentansprüche

1. Verfahren zur Herstellung eines G-CSF-Analogs, welches die Schritte umfaßt:

   (a) Betrachten, auf dem Aminosäure- oder Atomniveau, von Information, welche die dreidimensionale Struktur eines G-CSF-Moleküls, wie angegeben in Fig. 5, vermittelt;

   (b) Auswählen, aus besagter betrachteten Information, von wenigstens einer Stelle auf besagtem G-CSF-Molekül für eine Veränderung;

   (c) Herstellen eines G-CSF-Moleküls mit einer solchen Veränderung; und

   (d) fakultativ, Testen eines solchen G-CSF-Moleküls auf eine gewünschte Eigenschaft.

2. Verfahren zur Herstellung eines G-CSF-Analogs nach Anspruch 1, auf der Basis der Verwendung eines Compu-

ters, welches die Schritte umfaßt:

(a) Bereitstellen einer Computerdarstellung, auf dem Aminosäure- oder Atomniveau, der dreidimensionalen Struktur eines G-CSF-Moleküls, wie angegeben in Fig. 5;

(b) Auswählen, aus besagter Computerdarstellung, von wenigstens einer Stelle auf besagtem G-CSF-Molekül für eine Veränderung;

(c) Herstellen eines G-CSF-Moleküls mit einer solchen Veränderung; und

(d) fakultativ, Testen eines solchen G-CSF-Moleküls auf eine gewünschte Eigenschaft.

3. Verfahren zur Herstellung eines G-CSF-Analogs nach Anspruch 2, welches umfaßt:

(a) Versehen besagten Computers mit Mitteln zum Anzeigen der dreidimensionalen Struktur eines G-CSF-Moleküls, wie angegeben in Fig. 5, einschließlich Anzeigen der Zusammensetzung der Einheiten besagten G-CSF-Moleküls, vorzugsweise Anzeigen der dreidimensionalen Anordnung jeder Aminosäure und bevorzugter Anzeigen der dreidimensionalen Anordnung jedes Atoms eines G-CSF-Moleküls;

(b) Betrachten besagter Ansicht;

(c) Auswählen einer Stelle auf besagter Ansicht für eine Veränderung in der Zusammensetzung besagten Moleküls oder der Anordnung einer Einheit; und

(d) Herstellen eines G-CSF-Analogs mit solch einer Änderung.

4. Computergestütztes Verfahren zur Herstellung eines G-CSF-Analogs, welches die Schritte umfaßt:

(a) Betrachten, auf dem Aminosäure- oder Atomniveau, der dreidimensionalen Struktur eines G-CSF-Moleküls, wie angegeben in Fig. 5, über einen Computer, wobei besagter Computer zuvor so programmiert worden ist, daß er (i) die Koordinaten eines G-CSF-Moleküls im dreidimensionalen Raum darstellt und (ii) die Eingabe von Information zur Veränderung besagter G-CSF-Darstellung und Betrachtung derselben ermöglicht;

(b) Auswählen einer Stelle auf besagtem visuellen Bild besagten G-CSF-Moleküls für eine Veränderung;

(c) Eingeben der Information für besagte Veränderung in besagten Computer;

(d) Betrachten einer dreidimensionalen Struktur besagten veränderten G-CSF-Moleküls über besagten Computer;

(e) fakultativ, Wiederholen der Schritte (a) - (e) oben;

(f) Herstellen eines G-CSF-Analogs mit besagter Veränderung; und

(g) fakultativ, Testen besagten G-CSF-Analogs auf eine gewünschte Eigenschaft.

Revendications

1. Procédé pour préparer un analogue de G-CSF, comprenant les étapes de :

(a) visualiser au niveau atomique ou des acides aminés des informations fournissant la structure tridimensionnelle d'une molécule de G-CSF comme indiqué sur la figure 5,
(b) choisir à partir desdites informations visualisées au moins un site sur ladite molécule de G-CSF pour altération ;
(c) préparer une molécule de G-CSF ayant une telle altération ; et
(d) éventuellement, tester une telle molécule de G-CSF en ce qui concerne une caractéristique souhaitée.

2. Procédé pour préparer un analogue de G-CSF selon la revendication 1, basé sur l'utilisation d'un ordinateur, com-

prenant les étapes de :

(a) fournir l'expression par ordinateur au niveau atomique ou des acides aminés de la structure tridimensionnelle d'une molécule de G-CSF comme indiqué sur la figure 5,
(b) choisir à partir de ladite expression par ordinateur au moins un site sur ladite molécule de G-CSF pour altération ;
(c) préparer une molécule de G-CSF ayant une telle altération ; et
(d) éventuellement, tester une telle molécule de G-CSF en ce qui concerne une caractéristique souhaitée.

3. Procédé pour préparer un analogue de G-CSF selon la revendication 2, comprenant :

(a) munir ledit ordinateur des moyens pour afficher la structure tridimensionnelle d'une molécule de G-CSF comme indiqué sur la figure 5 incluant l'affichage de la composition des fractions de ladite molécule de G-CSF, en affichant de préférence l'emplacement tridimensionnel de chaque acide aminé, et, plus préférablement, en affichant l'emplacement tridimensionnel de chaque atome d'une molécule de G-CSF ;
(b) visualiser ledit affichage ;
(c) choisir un site sur ledit affichage pour altération de la composition de ladite molécule ou de l'emplacement d'une fraction ; et
(d) préparer un analogue de G-CSF ayant une telle altération.

4. Procédé assisté par ordinateur pour préparer un analogue de G-CSF, comprenant les étapes de :

(a) visualiser au niveau atomique ou des acides aminés la structure tridimensionnelle d'une molécule de G-CSF comme indiqué sur la figure 5 via un ordinateur, ledit ordinateur ayant été préalablement programmé (i) pour exprimer les coordonnées d'une molécule de G-CSF dans l'espace tridimensionnel, et (ii) pour permettre l'entrée des informations pour l'altération de ladite expression de G-CSF et sa visualisation ;
(b) choisir un site sur ladite image visuelle de ladite molécule de G-CSF pour altération ;
(c) entrer des informations pour ladite altération dans ledit ordinateur ;
(d) visualiser une structure tridimensionnelle de ladite molécule de G-CSF altérée via ledit ordinateur ;
(e) répéter éventuellement les étapes (a) - (e) ci-dessus ;
(f) préparer un analogue de G-CSF ayant ladite altération ; et
(g) tester éventuellement ledit analogue de G-CSF en ce qui concerne une caractéristique souhaitée.

```
                                                Met Thr Pro Leu Gly Pro Ala
TCTAGAAAAAACCAAGGAGGTAATAAATA ATG ACT CCA TTA GGT CCT GCT

Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu Gln
TCT TCT CTG CCG CAA AGC TTT CTG CTG AAA TGT CTG GAA CAG

Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu
GTT CGT AAA ATC CAG GGT GAC GGT GCT GCA CTG CAA GAA AAA CTG

Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu
TGC GCT ACT TAC AAA CTG TGC CAT CCG GAA GAG CTG GTA CTG CTG

Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro
GGT CAT TCT CTT GGG ATC CCG TGG GCT CCG CTG TCT TCT TGT CCA

Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
TCT CAA GCT CTT CAG CTG GCT GGT TGT CTG TCT CAA CTG CAT TCT

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
GGT CTG TTC CTG TAT CAG GGT CTT CTG CAA GCT CTG GAA GGT ATC

Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val
TCT CCG GAA CTG GGT CCG ACT CTG GAC ACT CTG CAG CTA GAT GTA

Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly
GCT GAC TTT GCT ACT ACT ATT TGG CAA CAG ATG GAA GAG CTC GGT

Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe
ATG GCA CCA GCT CTG CAA CCG ACT CAA GGT GCT ATG CCG GCA TTC

Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser
GCT TCT GCA TTC CAG CGT CGT GCA GGA GGT GTA CTG GTT GCT TCT

His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His
CAT CTG CAA TCT TTC CTG GAA GTA TCT TAC CGT GTT CTG CGT CAT

Leu Ala Gln Pro OC  AM
CTG GCT CAG CCG TAA TAG AATTC
```

FIGURE 1

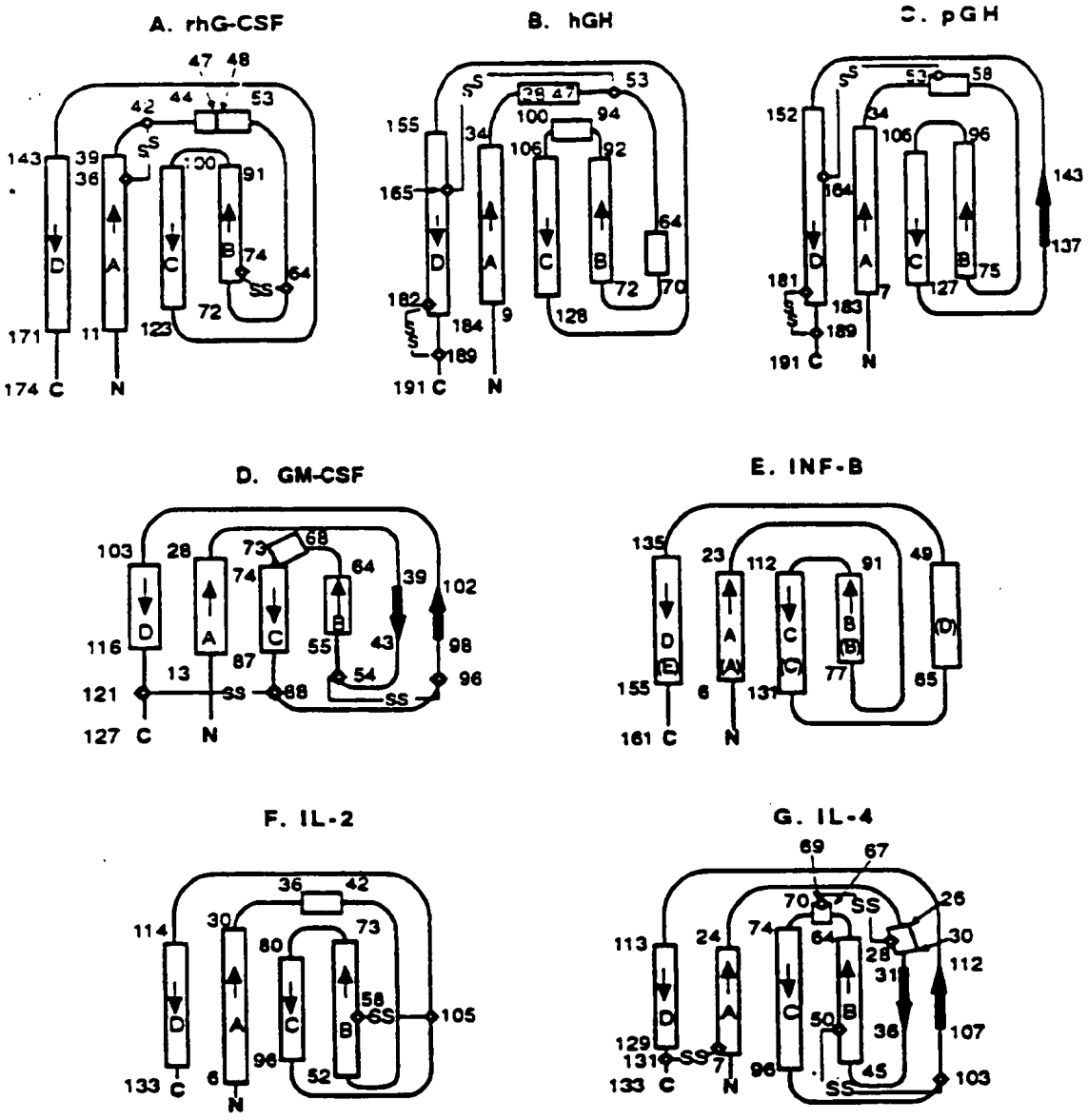

FIGURE 2

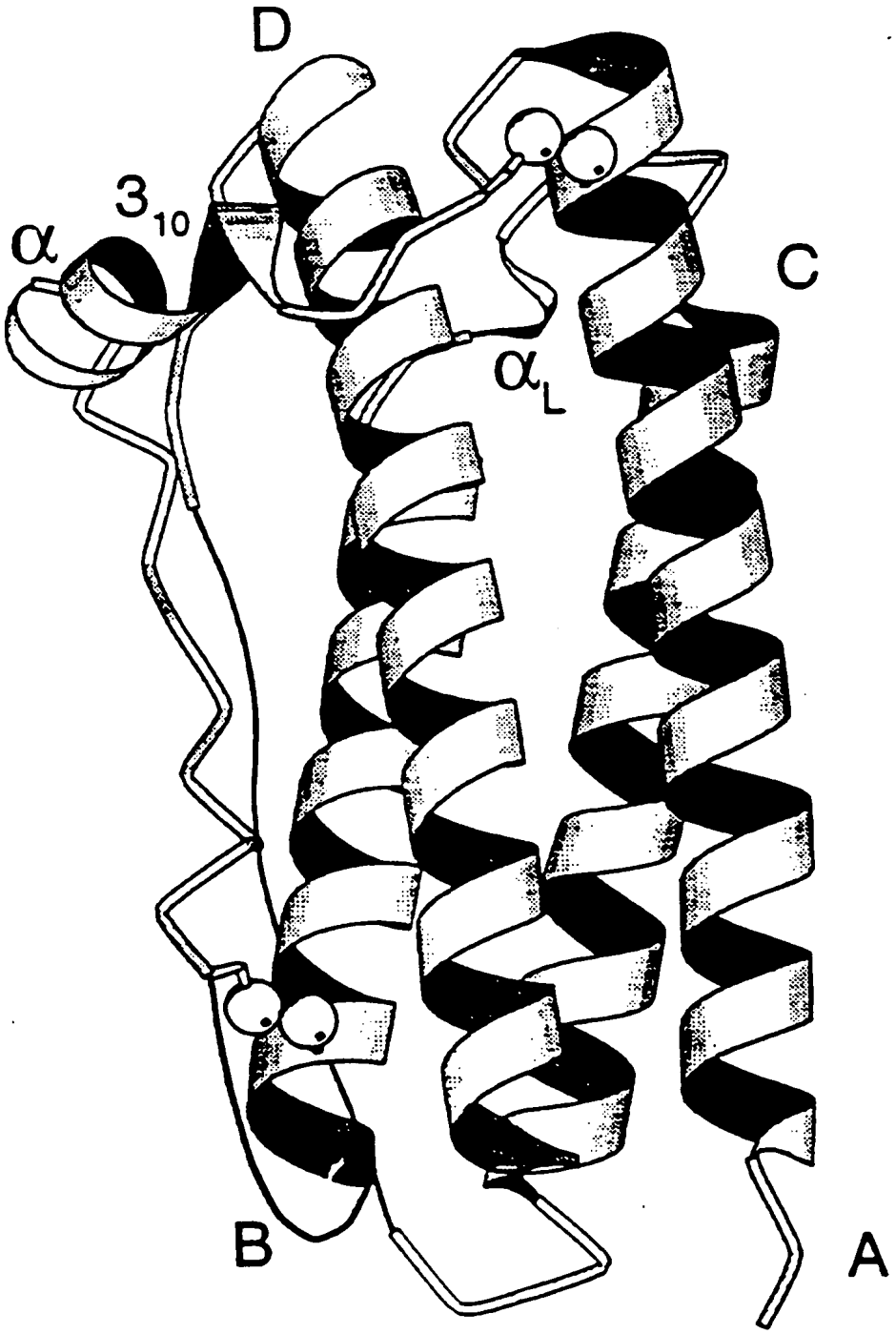

FIGURE 3

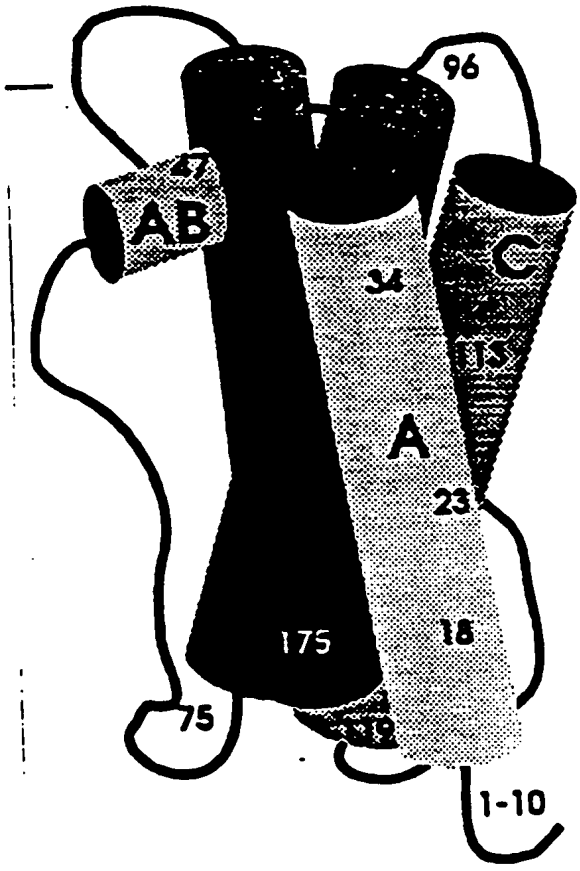

FIGURE 4

FIGURE 5

```
ATOM    1 CB  LEU   10     58.751  58.191 -14.868  1.00 61.22      A1
ATOM    2 CG  LEU   10     58.360  59.271 -13.939  1.00 60.19      A1
ATOM    3 CD1 LEU   10     59.307  60.461 -14.022  1.00 60.14      A1
ATOM    4 CD2 LEU   10     56.954  59.658 -14.335  1.00 60.68      A1
ATOM    5 C   LEU   10     60.544  56.734 -13.849  1.00 62.85      A1
ATOM    6 O   LEU   10     60.079  55.595 -14.041  1.00 63.08      A1
ATOM    7 HT1 LEU   10     59.876  56.135 -15.998  1.00  0.00      A1
ATOM    8 HT2 LEU   10     61.323  56.887 -16.434  1.00  0.00      A1
ATOM    9 N   LEU   10     60.328  57.059 -16.204  1.00 62.24      A1
ATOM   10 HT3 LEU   10     59.817  57.535 -16.971  1.00  0.00      A1
ATOM   11 CA  LEU   10     60.183  57.758 -14.941  1.00 62.58      A1
ATOM   12 N   PRO   11     61.357  56.962 -12.780  1.00 61.96      A1
ATOM   13 CD  PRO   11     61.960  58.238 -12.383  1.00 61.21      A1
ATOM   14 CA  PRO   11     61.832  55.889 -11.906  1.00 61.34      A1
ATOM   15 CB  PRO   11     62.915  56.547 -11.043  1.00 59.77      A1
ATOM   16 CG  PRO   11     62.511  57.983 -10.975  1.00 59.16      A1
ATOM   17 C   PRO   11     60.712  55.225 -11.109  1.00 60.68      A1
ATOM   18 O   PRO   11     60.075  55.843 -10.250  1.00 61.73      A1
ATOM   19 N   GLN   12     60.466  53.946 -11.407  1.00 59.31      A1
ATOM   20 H   GLN   12     60.944  53.573 -12.175  1.00  0.00      A1
ATOM   21 CA  GLN   12     59.468  53.121 -10.743  1.00 57.22      A1
ATOM   22 CB  GLN   12     59.779  51.646 -10.970  1.00 59.27      A1
ATOM   23 CG  GLN   12     58.620  50.714 -10.591  1.00 59.70      A1
ATOM   24 CD  GLN   12     57.604  50.575 -11.702  1.00 61.71      A1
ATOM   25 OE1 GLN   12     57.170  49.465 -11.970  1.00 65.82      A1
ATOM   26 NE2 GLN   12     57.227  51.534 -12.541  1.00 63.02      A1
ATOM   27 HE21 GLN  12     57.639  52.419 -12.489  1.00  0.00      A1
ATOM   28 HE22 GLN  12     56.500  51.308 -13.156  1.00  0.00      A1
ATOM   29 C   GLN   12     59.336  53.347  -9.245  1.00 55.34      A1
ATOM   30 O   GLN   12     58.242  53.196  -8.708  1.00 54.56      A1
ATOM   31 N   SER   13     60.423  53.732  -8.576  1.00 53.44      A1
ATOM   32 H   SER   13     61.276  53.839  -9.033  1.00  0.00      A1
ATOM   33 CA  SER   13     60.335  53.974  -7.168  1.00 52.86      A1

ATOM   34 CB  SER   13     61.704  54.144  -6.626  1.00 52.24      A1
ATOM   35 OG  SER   13     61.702  53.493  -5.362  1.00 56.64      A1
ATOM   36 HG  SER   13     61.534  52.551  -5.477  1.00  0.00      A1
ATOM   37 C   SER   13     59.497  55.214  -6.900  1.00 52.58      A1
ATOM   38 O   SER   13     58.509  55.144  -6.160  1.00 53.55      A1
ATOM   39 N   PHE   14     59.791  56.333  -7.577  1.00 50.84      A1
ATOM   40 H   PHE   14     60.469  56.292  -8.279  1.00  0.00      A1
ATOM   41 CA  PHE   14     59.067  57.590  -7.423  1.00 47.21      A1
ATOM   42 CB  PHE   14     59.611  58.590  -8.454  1.00 44.68      A1
ATOM   43 CG  PHE   14     58.618  59.669  -8.866  1.00 42.88      A1
ATOM   44 CD1 PHE   14     58.052  59.594 -10.123  1.00 40.40      A1
ATOM   45 CD2 PHE   14     58.264  60.673  -7.978  1.00 40.30      A1
ATOM   46 CE1 PHE   14     57.114  60.518 -10.507  1.00 39.59      A1
ATOM   47 CE2 PHE   14     57.329  61.587  -8.380  1.00 41.82      A1
ATOM   48 CZ  PHE   14     56.751  61.515  -9.635  1.00 41.56      A1
ATOM   49 C   PHE   14     57.605  57.263  -7.661  1.00 45.83      A1

ATOM   50 O   PHE   14     56.789  57.588  -6.805  1.00 46.07      A1
ATOM   51 N   LEU   15     57.298  56.509  -8.718  1.00 44.64      A1
ATOM   52 H   LEU   15     58.024  56.183  -9.287  1.00  0.00      A1
ATOM   53 CA  LEU   15     55.940  56.181  -9.038  1.00 44.53      A1
ATOM   54 CB  LEU   15     55.858  55.402 -10.300  1.00 48.75      A1
ATOM   55 CG  LEU   15     54.853  56.013 -11.289  1.00 51.65      A1
ATOM   56 CD1 LEU   15     55.525  57.121 -12.105  1.00 50.33      A1
ATOM   57 CD2 LEU   15     54.320  54.906 -12.204  1.00 53.77      A1
ATOM   58 C   LEU   15     55.169  55.410  -8.014  1.00 44.07      A1
ATOM   59 O   LEU   15     53.945  55.567  -7.959  1.00 45.46      A1
ATOM   60 N   LEU   16     55.809  54.620  -7.166  1.00 43.18      A1
ATOM   61 H   LEU   16     56.781  54.503  -7.251  1.00  0.00      A1
ATOM   62 CA  LEU   16     55.110  53.913  -6.095  1.00 42.96      A1
ATOM   63 CB  LEU   16     55.866  52.623  -5.751  1.00 43.44      A1
ATOM   64 CG  LEU   16     55.840  51.608  -6.868  1.00 42.25      A1
ATOM   65 CD1 LEU   16     56.889  50.567  -6.596  1.00 43.68      A1
ATOM   66 CD2 LEU   16     54.413  51.068  -7.030  1.00 42.75      A1
ATOM   67 C   LEU   16     54.963  54.778  -4.852  1.00 42.35      A1
ATOM   68 O   LEU   16     54.077  54.579  -4.018  1.00 42.65      A1
ATOM   69 N   LYS   17     55.823  55.779  -4.703  1.00 42.47      A1
ATOM   70 H   LYS   17     56.587  55.840  -5.320  1.00  0.00      A1
ATOM   71 CA  LYS   17     55.681  56.767  -3.650  1.00 42.07      A1
ATOM   72 CB  LYS   17     56.995  57.554  -3.573  1.00 44.14      A1
ATOM   73 CG  LYS   17     57.214  58.197  -2.223  1.00 49.61      A1
ATOM   74 CD  LYS   17     57.114  57.164  -1.086  1.00 55.15      A1
ATOM   75 CE  LYS   17     56.747  57.804   0.293  1.00 62.05      A1
ATOM   76 NZ  LYS   17     55.462  58.533   0.331  1.00 65.43      A1
ATOM   77 HZ1 LYS   17     54.684  57.884   0.098  1.00  0.00      A1
ATOM   78 HZ2 LYS   17     55.482  59.308  -0.362  1.00  0.00      A1
ATOM   79 HZ3 LYS   17     55.312  58.926   1.282  1.00  0.00      A1
ATOM   80 C   LYS   17     54.463  57.640  -4.051  1.00 41.20      A1
ATOM   81 O   LYS   17     53.648  57.999  -3.186  1.00 40.66      A1
ATOM   82 N   CYS   18     54.272  57.992  -5.346  1.00 39.13      A1
ATOM   83 H   CYS   18     54.998  57.809  -5.981  1.00  0.00      A1
ATOM   84 CA  CYS   18     53.080  58.656  -5.802  1.00 37.42      A1
ATOM   85 CB  CYS   18     53.092  58.891  -7.261  1.00 38.02      A1
ATOM   86 SG  CYS   18     54.421  60.026  -7.681  1.00 40.40      A1
ATOM   87 C   CYS   18     51.859  57.789  -5.502  1.00 39.33      A1
ATOM   88 O   CYS   18     50.959  58.346  -4.847  1.00 40.89      A1
ATOM   89 N   LEU   19     51.738  56.475  -5.842  1.00 37.15      A1
ATOM   90 H   LEU   19     52.462  56.038  -6.341  1.00  0.00      A1
ATOM   91 CA  LEU   19     50.521  55.702  -5.534  1.00 36.00      A1
ATOM   92 CB  LEU   19     50.644  54.204  -5.947  1.00 38.31      A1
ATOM   93 CG  LEU   19     49.410  53.271  -5.657  1.00 40.86      A1
ATOM   94 CD1 LEU   19     48.208  53.684  -6.467  1.00 39.71      A1
ATOM   95 CD2 LEU   19     49.692  51.833  -6.113  1.00 45.71      A1
ATOM   96 C   LEU   19     50.102  55.736  -4.076  1.00 33.52      A1
ATOM   97 O   LEU   19     48.930  55.949  -3.766  1.00 32.75      A1
ATOM   98 N   GLU   20     51.030  55.576  -3.166  1.00 31.88      A1
ATOM   99 H   GLU   20     51.940  55.338  -3.455  1.00  0.00      A1
ATOM  100 CA  GLU   20     50.750  55.710  -1.748  1.00 31.40      A1
```

FIGURE 5

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ATOM  101  CB  GLU   20      52.053  55.334  -1.167  1.00 35.25      A1
ATOM  102  CG  GLU   20      52.508  55.504   0.260  1.00 43.21      A1
ATOM  103  CD  GLU   20      53.948  54.947   0.407  1.00 51.06      A1
ATOM  104  OE1 GLU   20      54.320  54.660   1.546  1.00 56.78      A1
ATOM  105  OE2 GLU   20      54.708  54.766  -0.570  1.00 51.57      A1
ATOM  106  C   GLU   20      50.230  57.117  -1.326  1.00 33.25      A1
ATOM  107  O   GLU   20      49.432  57.291  -0.380  1.00 33.30      A1
ATOM  108  N   GLN   21      50.660  58.167  -2.044  1.00 32.33      A1
ATOM  109  H   GLN   21      51.270  58.004  -2.794  1.00  0.00      A1
ATOM  110  CA  GLN   21      50.275  59.538  -1.742  1.00 31.00      A1
ATOM  111  CB  GLN   21      51.326  60.489  -2.340  1.00 32.37      A1
ATOM  112  CG  GLN   21      52.436  60.530  -1.272  1.00 38.01      A1
ATOM  113  CD  GLN   21      53.622  61.460  -1.504  1.00 42.67      A1
ATOM  114  OE1 GLN   21      54.008  62.236  -0.615  1.00 43.63      A1
ATOM  115  NE2 GLN   21      54.256  61.448  -2.678  1.00 42.31      A1
ATOM  116 HE21 GLN   21      53.965  60.840  -3.384  1.00  0.00      A1
ATOM  117 HE22 GLN   21      55.026  62.052  -2.730  1.00  0.00      A1
ATOM  118  C   GLN   21      48.894  59.765  -2.288  1.00 28.51      A1
ATOM  119  O   GLN   21      48.027  60.242  -1.563  1.00 28.65      A1
ATOM  120  N   VAL   22      48.682  59.319  -3.521  1.00 25.85      A1
ATOM  121  H   VAL   22      49.448  58.980  -4.013  1.00  0.00      A1
ATOM  122  CA  VAL   22      47.382  59.303  -4.161  1.00 24.94      A1
ATOM  123  CB  VAL   22      47.508  58.614  -5.526  1.00 24.09      A1
ATOM  124  CG1 VAL   22      46.154  58.378  -6.096  1.00 19.97      A1
ATOM  125  CG2 VAL   22      48.252  59.479  -6.498  1.00 25.82      A1
ATOM  126  C   VAL   22      46.418  58.549  -3.226  1.00 25.65      A1
ATOM  127  O   VAL   22      45.428  59.190  -2.800  1.00 29.31      A1
ATOM  128  N   ARG   23      46.643  57.291  -2.759  1.00 23.93      A1
ATOM  129  H   ARG   23      47.440  56.819  -3.056  1.00  0.00      A1
ATOM  130  CA  ARG   23      45.667  56.593  -1.892  1.00 20.67      A1
ATOM  131  CB  ARG   23      46.104  55.135  -1.635  1.00 20.45      A1
ATOM  132  CG  ARG   23      46.325  54.321  -2.904  1.00 17.51      A1
ATOM  133  CD  ARG   23      45.095  54.446  -3.769  1.00 21.54      A1
ATOM  134  NE  ARG   23      45.076  53.437  -4.809  1.00 24.82      A1
ATOM  135  HE  ARG   23      45.642  52.647  -4.701  1.00  0.00      A1
ATOM  136  CZ  ARG   23      44.323  53.556  -5.904  1.00 27.69      A1
ATOM  137  NH1 ARG   23      43.567  54.669  -6.006  1.00 29.51      A1
ATOM  138 HH11 ARG   23      43.562  55.377  -5.303  1.00  0.00      A1
ATOM  139 HH12 ARG   23      42.956  54.730  -6.789  1.00  0.00      A1
ATOM  140  NH2 ARG   23      44.345  52.604  -6.891  1.00 24.22      A1
ATOM  141 HH21 ARG   23      43.780  52.713  -7.709  1.00  0.00      A1
ATOM  142 HH22 ARG   23      44.936  51.802  -6.793  1.00  0.00      A1
ATOM  143  C   ARG   23      45.458  57.285  -0.560  1.00 20.56      A1
ATOM  144  O   ARG   23      44.374  57.254   0.042  1.00 20.04      A1
ATOM  145  N   LYS   24      46.485  58.015  -0.118  1.00 22.67      A1
ATOM  146  H   LYS   24      47.291  58.105  -0.668  1.00  0.00      A1
ATOM  147  CA  LYS   24      46.431  58.729   1.166  1.00 22.85      A1
ATOM  148  CB  LYS   24      47.811  59.255   1.506  1.00 26.86      A1
ATOM  149  CG  LYS   24      47.821  59.661   2.971  1.00 33.79      A1
ATOM  150  CD  LYS   24      49.121  60.265   3.404  1.00 40.73      A1
ATOM  151  CE  LYS   24      50.258  59.258   3.335  1.00 46.19      A1
ATOM  152  NZ  LYS   24      51.532  59.975   3.333  1.00 51.19      A1
ATOM  153 HZ1 LYS   24      51.627  60.498   4.225  1.00  0.00      A1
ATOM  154 HZ2 LYS   24      51.539  60.651   2.539  1.00  0.00      A1
ATOM  155 HZ3 LYS   24      52.317  59.303   3.216  1.00  0.00      A1
ATOM  156  C   LYS   24      45.455  59.893   1.101  1.00 21.66      A1
ATOM  157  O   LYS   24      44.588  60.068   1.962  1.00 20.90      A1
ATOM  158  N   ILE   25      45.549  60.696   0.044  1.00 21.46      A1
ATOM  159  H   ILE   25      46.242  60.509  -0.629  1.00  0.00      A1
ATOM  160  CA  ILE   25      44.667  61.841  -0.115  1.00 22.53      A1
ATOM  161  CB  ILE   25      45.075  62.694  -1.307  1.00 22.15      A1
ATOM  162  CG2 ILE   25      44.097  63.834  -1.439  1.00 20.44      A1
ATOM  163  CG1 ILE   25      46.475  63.230  -1.136  1.00 21.03      A1
ATOM  164  CD  ILE   25      47.188  63.281  -2.497  1.00 20.04      A1
ATOM  165  C   ILE   25      43.263  61.308  -0.352  1.00 24.75      A1
ATOM  166  O   ILE   25      42.339  61.839   0.301  1.00 26.13      A1
ATOM  167  N   GLN   26      43.065  60.289  -1.244  1.00 22.79      A1
ATOM  168  H   GLN   26      43.842  59.926  -1.726  1.00  0.00      A1
ATOM  169  CA  GLN   26      41.737  59.713  -1.437  1.00 20.12      A1
ATOM  170  CB  GLN   26      41.729  58.539  -2.341  1.00 18.89      A1
ATOM  171  CG  GLN   26      42.203  59.042  -3.627  1.00 19.77      A1
ATOM  172  CD  GLN   26      42.163  57.996  -4.684  1.00 24.26      A1
ATOM  173  OE1 GLN   26      42.550  56.853  -4.465  1.00 25.82      A1
ATOM  174  NE2 GLN   26      41.732  58.351  -5.890  1.00 27.68      A1
ATOM  175 HE21 GLN   26      41.421  59.265  -6.042  1.00  0.00      A1
ATOM  176 HE22 GLN   26      41.743  57.649  -6.552  1.00  0.00      A1
ATOM  177  C   GLN   26      41.207  59.239  -0.111  1.00 21.68      A1
ATOM  178  O   GLN   26      40.067  59.550   0.220  1.00 27.02      A1
ATOM  179  N   GLY   27      41.952  58.622   0.773  1.00 22.54      A1
ATOM  180  H   GLY   27      42.891  58.420   0.576  1.00  0.00      A1
ATOM  181  CA  GLY   27      41.386  58.191   2.037  1.00 25.55      A1
ATOM  182  C   GLY   27      40.936  59.352   2.890  1.00 27.80      A1
ATOM  183  O   GLY   27      39.889  59.251   3.526  1.00 29.95      A1
ATOM  184  N   ASP   28      41.683  60.460   2.915  1.00 29.39      A1
ATOM  185  H   ASP   28      42.547  60.454   2.448  1.00  0.00      A1
ATOM  186  CA  ASP   28      41.257  61.680   3.624  1.00 28.95      A1
ATOM  187  CB  ASP   28      42.266  62.789   3.552  1.00 30.13      A1
ATOM  188  CG  ASP   28      43.737  62.502   3.777  1.00 31.72      A1
ATOM  189  OD1 ASP   28      44.539  63.074   2.995  1.00 31.95      A1
ATOM  190  OD2 ASP   28      44.063  61.811   4.741  1.00 32.60      A1
ATOM  191  C   ASP   28      39.994  62.264   2.960  1.00 25.81      A1
ATOM  192  O   ASP   28      39.101  62.699   3.655  1.00 26.21      A1
ATOM  193  N   GLY   29      39.882  62.270   1.631  1.00 23.93      A1
ATOM  194  H   GLY   29      40.660  61.950   1.135  1.00  0.00      A1
ATOM  195  CA  GLY   29      38.729  62.694   0.886  1.00 25.69      A1
ATOM  196  C   GLY   29      37.528  61.961   1.418  1.00 27.36      A1
ATOM  197  O   GLY   29      36.648  62.558   2.061  1.00 28.14      A1
ATOM  198  N   ALA   30      37.646  60.628   1.295  1.00 27.85      A1
ATOM  199  H   ALA   30      38.442  60.288   0.843  1.00  0.00      A1
ATOM  200  CA  ALA   30      36.683  59.655   1.814  1.00 25.94      A1
ATOM  201  CB  ALA   30      37.269  58.303   1.556  1.00 22.15      A1
ATOM  202  C   ALA   30      36.356  59.842   3.308  1.00 27.18      A1
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FIGURE 5

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ATOM  203 O   ALA  30    35.194 59.772  3.754 1.00 28.82    A1
ATOM  204 N   ALA  31    37.340 60.105  4.150 1.00 27.16    A1
ATOM  205 H   ALA  31    38.253 60.114  3.809 1.00  0.00    A1
ATOM  206 CA  ALA  31    37.113 60.470  5.531 1.00 27.70    A1
ATOM  207 CB  ALA  31    38.383 60.881  6.177 1.00 27.65    A1
ATOM  208 C   ALA  31    36.178 61.675  5.660 1.00 30.01    A1
ATOM  209 O   ALA  31    35.195 61.624  6.413 1.00 32.91    A1
ATOM  210 N   LEU  32    36.397 62.744  4.895 1.00 27.63    A1
ATOM  211 H   LEU  32    37.133 62.734  4.242 1.00  0.00    A1
ATOM  212 CA  LEU  32    35.560 63.898  4.997 1.00 28.52    A1
ATOM  213 CB  LEU  32    36.226 65.019  4.167 1.00 32.94    A1
ATOM  214 CG  LEU  32    35.658 66.472  4.091 1.00 32.54    A1
ATOM  215 CD1 LEU  32    35.516 67.082  5.499 1.00 32.87    A1
ATOM  216 CD2 LEU  32    36.555 67.267  3.181 1.00 30.97    A1
ATOM  217 C   LEU  32    34.133 63.597  4.518 1.00 27.87    A1
ATOM  218 O   LEU  32    33.169 63.889  5.250 1.00 25.93    A1
ATOM  219 N   GLN  33    33.977 63.028  3.315 1.00 27.51    A1
ATOM  220 H   GLN  33    34.787 62.826  2.802 1.00  0.00    A1
ATOM  221 CA  GLN  33    32.687 62.671  2.775 1.00 30.40    A1
ATOM  222 CB  GLN  33    32.737 61.721  1.614 1.00 29.47    A1
ATOM  223 CG  GLN  33    32.888 62.584  0.436 1.00 29.26    A1
ATOM  224 CD  GLN  33    33.015 61.869 -0.887 1.00 30.21    A1
ATOM  225 OE1 GLN  33    34.064 61.495 -1.452 1.00 29.61    A1
ATOM  226 NE2 GLN  33    31.823 61.759 -1.426 1.00 33.19    A1
ATOM  227 HE21 GLN  33    31.781 61.328 -2.302 1.00  0.00    A1
ATOM  228 HE22 GLN  33    31.042 62.060 -0.914 1.00  0.00    A1
ATOM  229 C   GLN  33    31.839 61.963  3.788 1.00 35.60    A1
ATOM  230 O   GLN  33    30.715 62.416  4.073 1.00 36.49    A1
ATOM  231 N   GLU  34    32.386 60.925  4.438 1.00 39.81    A1
ATOM  232 H   GLU  34    33.340 60.707  4.328 1.00  0.00    A1
ATOM  233 CA  GLU  34    31.541 60.131  5.304 1.00 43.24    A1
ATOM  234 CB  GLU  34    32.228 58.792  5.571 1.00 46.46    A1
ATOM  235 CG  GLU  34    33.274 58.721  6.624 1.00 55.01    A1
ATOM  236 CD  GLU  34    32.777 58.092  7.930 1.00 60.29    A1
ATOM  237 OE1 GLU  34    33.483 57.186  8.412 1.00 63.26    A1
ATOM  238 OE2 GLU  34    31.724 58.504  8.459 1.00 60.44    A1
ATOM  239 C   GLU  34    31.218 60.877  6.564 1.00 43.59    A1
ATOM  240 O   GLU  34    30.175 60.631  7.161 1.00 44.87    A1
ATOM  241 N   LYS  35    32.045 61.811  6.998 1.00 44.80    A1
ATOM  242 H   LYS  35    32.923 61.931  6.569 1.00  0.00    A1
ATOM  243 CA  LYS  35    31.674 62.634  8.134 1.00 45.43    A1
ATOM  244 CB  LYS  35    32.881 63.364  8.686 1.00 47.67    A1
ATOM  245 CG  LYS  35    33.701 62.414  9.510 1.00 52.75    A1
ATOM  246 CD  LYS  35    35.084 63.021  9.548 1.00 57.55    A1
ATOM  247 CE  LYS  35    36.067 62.099 10.238 1.00 60.35    A1
ATOM  248 NZ  LYS  35    35.810 62.064 11.669 1.00 62.91    A1
ATOM  249 HZ1 LYS  35    34.838 61.733 11.840 1.00  0.00    A1
ATOM  250 HZ2 LYS  35    35.930 63.011 12.078 1.00  0.00    A1
ATOM  251 HZ3 LYS  35    36.477 61.405 12.119 1.00  0.00    A1
ATOM  252 C   LYS  35    30.630 63.660  7.697 1.00 44.45    A1
ATOM  253 O   LYS  35    29.730 63.999  8.478 1.00 44.61    A1
ATOM  254 N   LEU  36    30.652 64.190  6.480 1.00 41.21    A1
ATOM  255 H   LEU  36    31.343 63.930  5.836 1.00  0.00    A1
ATOM  256 CA  LEU  36    29.647 65.157  6.144 1.00 40.25    A1
ATOM  257 CB  LEU  36    30.070 65.899  4.889 1.00 39.01    A1
ATOM  258 CG  LEU  36    31.253 66.834  4.935 1.00 38.99    A1
ATOM  259 CD1 LEU  36    31.438 67.404  3.571 1.00 42.08    A1
ATOM  260 CD2 LEU  36    31.034 67.939  5.928 1.00 35.05    A1
ATOM  261 C   LEU  36    28.332 64.414  5.941 1.00 41.90    A1
ATOM  262 O   LEU  36    27.267 64.828  6.431 1.00 42.30    A1
ATOM  263 N   CYS  37    28.392 63.251  5.309 1.00 42.63    A1
ATOM  264 H   CYS  37    29.250 62.904  5.020 1.00  0.00    A1
ATOM  265 CA  CYS  37    27.216 62.469  5.084 1.00 43.54    A1
ATOM  266 C   CYS  37    26.638 62.026  6.362 1.00 44.65    A1
ATOM  267 O   CYS  37    25.426 61.997  6.459 1.00 46.40    A1
ATOM  268 CB  CYS  37    27.474 61.240  4.313 1.00 44.60    A1
ATOM  269 SG  CYS  37    26.133 60.038  4.530 1.00 43.86    A1
ATOM  270 N   ALA  38    27.465 61.734  7.342 1.00 45.96    A1
ATOM  271 H   ALA  38    28.433 61.707  7.202 1.00  0.00    A1
ATOM  272 CA  ALA  38    26.932 61.261  8.592 1.00 48.03    A1
ATOM  273 CB  ALA  38    27.869 60.140  9.108 1.00 48.64    A1
ATOM  274 C   ALA  38    26.748 62.358  9.624 1.00 48.89    A1
ATOM  275 O   ALA  38    26.103 62.085 10.621 1.00 50.72    A1
ATOM  276 N   THR  39    27.256 63.590  9.512 1.00 50.66    A1
ATOM  277 H   THR  39    27.858 63.780  8.770 1.00  0.00    A1
ATOM  278 CA  THR  39    26.976 64.638 10.503 1.00 51.54    A1
ATOM  279 CB  THR  39    28.179 65.593 10.690 1.00 51.76    A1
ATOM  280 OG1 THR  39    29.294 64.826 11.126 1.00 52.65    A1
ATOM  281 HG1 THR  39    29.749 64.481 10.355 1.00  0.00    A1
ATOM  282 CG2 THR  39    27.900 66.655 11.729 1.00 51.62    A1
ATOM  283 C   THR  39    25.775 65.466 10.037 1.00 52.17    A1
ATOM  284 O   THR  39    24.886 65.882 10.781 1.00 52.15    A1
ATOM  285 N   TYR  40    25.751 65.720  8.738 1.00 52.83    A1
ATOM  286 H   TYR  40    26.420 65.331  8.139 1.00  0.00    A1
ATOM  287 CA  TYR  40    24.729 66.561  8.165 1.00 52.53    A1
ATOM  288 CB  TYR  40    25.314 67.872  7.696 1.00 52.15    A1
ATOM  289 CG  TYR  40    26.399 68.458  8.552 1.00 54.11    A1
ATOM  290 CD1 TYR  40    27.678 68.341  8.062 1.00 56.50    A1
ATOM  291 CE1 TYR  40    28.719 68.934  8.724 1.00 58.28    A1
ATOM  292 CD2 TYR  40    26.122 69.144  9.714 1.00 54.86    A1
ATOM  293 CE2 TYR  40    27.170 69.746 10.378 1.00 56.20    A1
ATOM  294 CZ  TYR  40    28.453 69.642  9.872 1.00 58.26    A1
ATOM  295 OH  TYR  40    29.513 70.310 10.463 1.00 61.00    A1
ATOM  296 HH  TYR  40    30.179 70.443  9.782 1.00  0.00    A1
ATOM  297 C   TYR  40    24.035 65.911  6.981 1.00 51.75    A1
ATOM  298 O   TYR  40    23.662 66.578  6.024 1.00 52.52    A1
ATOM  299 N   LYS  41    23.941 64.600  6.965 1.00 50.54    A1
ATOM  300 H   LYS  41    24.474 64.064  7.583 1.00  0.00    A1
ATOM  301 CA  LYS  41    23.112 63.885  6.029 1.00 50.48    A1
ATOM  302 CB  LYS  41    21.641 63.989  6.540 1.00 50.62    A1
ATOM  303 CG  LYS  41    21.387 63.326  7.911 1.00 52.11    A1
ATOM  304 CD  LYS  41    20.112 63.878  8.574 1.00 55.54    A1
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FIGURE 5

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ATOM  305 CE  LYS  41     19.578  63.087   9.820  1.00 58.79      A1
ATOM  306 NZ  LYS  41     18.374  63.648  10.457  1.00 58.31      A1
ATOM  307 HZ1 LYS  41     17.605  63.688   9.757  1.00  0.00      A1
ATOM  308 HZ2 LYS  41     18.578  64.607  10.803  1.00  0.00      A1
ATOM  309 HZ3 LYS  41     18.084  63.043  11.252  1.00  0.00      A1
ATOM  310 C   LYS  41     23.251  64.318   4.588  1.00 49.92      A1
ATOM  311 O   LYS  41     22.312  64.124   3.793  1.00 51.49      A1
ATOM  312 N   LEU  42     24.432  64.893   4.246  1.00 48.28      A1
ATOM  313 H   LEU  42     25.103  65.050   4.937  1.00  0.00      A1
ATOM  314 CA  LEU  42     24.742  65.286   2.859  1.00 46.61      A1
ATOM  315 CB  LEU  42     25.565  66.574   2.757  1.00 44.69      A1
ATOM  316 CG  LEU  42     24.807  67.802   3.218  1.00 42.63      A1
ATOM  317 CD1 LEU  42     25.718  68.580   4.097  1.00 43.29      A1
ATOM  318 CD2 LEU  42     24.283  68.590   2.045  1.00 41.26      A1
ATOM  319 C   LEU  42     25.580  64.124   2.397  1.00 45.46      A1
ATOM  320 O   LEU  42     26.766  64.017   2.711  1.00 46.32      A1
ATOM  321 N   CYS  43     24.882  63.193   1.754  1.00 44.09      A1
ATOM  322 H   CYS  43     23.925  63.353   1.619  1.00  0.00      A1
ATOM  323 CA  CYS  43     25.480  61.951   1.358  1.00 42.87      A1
ATOM  324 C   CYS  43     25.448  61.846  -0.123  1.00 41.62      A1
ATOM  325 O   CYS  43     25.762  60.805  -0.666  1.00 41.99      A1
ATOM  326 CB  CYS  43     24.716  60.796   2.026  1.00 41.77      A1
ATOM  327 SG  CYS  43     24.523  61.011   3.835  1.00 45.91      A1
ATOM  328 N   HIS  44     25.057  62.846  -0.882  1.00 42.90      A1
ATOM  329 H   HIS  44     24.841  63.721  -0.491  1.00  0.00      A1
ATOM  330 CA  HIS  44     25.069  62.680  -2.320  1.00 44.60      A1
ATOM  331 CB  HIS  44     23.653  62.764  -2.825  1.00 48.40      A1
ATOM  332 CG  HIS  44     23.085  60.935  -2.310  1.00 50.37      A1
ATOM  333 CD2 HIS  44     22.178  60.844  -1.272  1.00 50.52      A1
ATOM  334 ND1 HIS  44     23.358  59.689  -2.713  1.00 52.28      A1
ATOM  335 HD1 HIS  44     24.130  59.394  -3.251  1.00  0.00      A1
ATOM  336 CE1 HIS  44     22.652  58.873  -1.955  1.00 51.92      A1
ATOM  337 NE2 HIS  44     21.947  59.565  -1.091  1.00 50.53      A1
ATOM  338 HE2 HIS  44     21.290  59.189  -0.466  1.00  0.00      A1
ATOM  339 C   HIS  44     25.522  63.941  -3.047  1.00 43.69      A1
ATOM  340 O   HIS  44     24.765  64.906  -3.108  1.00 43.00      A1
ATOM  341 N   PRO  45     26.710  63.978  -3.667  1.00 43.07      A1
ATOM  342 CD  PRO  45     27.785  62.995  -3.501  1.00 42.17      A1
ATOM  343 CA  PRO  45     27.133  65.024  -4.570  1.00 42.50      A1
ATOM  344 CB  PRO  45     28.380  64.466  -5.217  1.00 39.76      A1
ATOM  345 CG  PRO  45     28.995  63.680  -4.123  1.00 39.09      A1
ATOM  346 C   PRO  45     26.071  65.423  -5.585  1.00 44.49      A1
ATOM  347 O   PRO  45     25.876  66.612  -5.801  1.00 45.36      A1
ATOM  348 N   GLU  46     25.334  64.501  -6.225  1.00 45.36      A1
ATOM  349 H   GLU  46     25.464  63.561  -5.996  1.00  0.00      A1
ATOM  350 CA  GLU  46     24.406  64.806  -7.319  1.00 45.46      A1
ATOM  351 CB  GLU  46     23.952  63.515  -7.997  1.00 50.54      A1
ATOM  352 CG  GLU  46     24.462  63.460  -9.445  1.00 58.48      A1
ATOM  353 CD  GLU  46     23.637  64.215 -10.502  1.00 64.93      A1
ATOM  354 OE1 GLU  46     23.642  65.455 -10.516  1.00 68.55      A1
ATOM  355 OE2 GLU  46     22.995  63.554 -11.332  1.00 68.31      A1
ATOM  356 C   GLU  46     23.181  65.584  -6.937  1.00 42.96      A1
ATOM  357 O   GLU  46     22.532  66.223  -7.748  1.00 41.71      A1
ATOM  358 N   GLU  47     22.919  65.563  -5.654  1.00 41.96      A1
ATOM  359 H   GLU  47     23.507  65.098  -5.028  1.00  0.00      A1
ATOM  360 CA  GLU  47     21.818  66.301  -5.144  1.00 43.21      A1
ATOM  361 CB  GLU  47     21.294  65.487  -3.963  1.00 43.24      A1
ATOM  362 CG  GLU  47     21.409  65.925  -2.515  1.00 46.07      A1
ATOM  363 CD  GLU  47     20.812  64.907  -1.547  1.00 47.86      A1
ATOM  364 OE1 GLU  47     19.847  64.225  -1.910  1.00 50.99      A1
ATOM  365 OE2 GLU  47     21.313  64.780  -0.427  1.00 49.47      A1
ATOM  366 C   GLU  47     22.295  67.718  -4.809  1.00 44.04      A1
ATOM  367 O   GLU  47     21.532  68.547  -4.292  1.00 44.60      A1
ATOM  368 N   LEU  48     23.567  68.015  -5.121  1.00 43.05      A1
ATOM  369 H   LEU  48     24.140  67.310  -5.465  1.00  0.00      A1
ATOM  370 CA  LEU  48     24.166  69.318  -4.904  1.00 42.42      A1
ATOM  371 CB  LEU  48     25.223  69.201  -3.858  1.00 40.56      A1
ATOM  372 CG  LEU  48     24.920  68.695  -2.489  1.00 41.87      A1
ATOM  373 CD1 LEU  48     26.277  68.424  -1.892  1.00 41.71      A1
ATOM  374 CD2 LEU  48     24.096  69.670  -1.633  1.00 41.13      A1
ATOM  375 C   LEU  48     24.792  69.937  -6.166  1.00 42.37      A1
ATOM  376 O   LEU  48     25.439  70.994  -6.098  1.00 42.37      A1
ATOM  377 N   VAL  49     24.566  69.366  -7.347  1.00 41.52      A1
ATOM  378 H   VAL  49     23.951  68.602  -7.362  1.00  0.00      A1
ATOM  379 CA  VAL  49     25.191  69.822  -8.578  1.00 41.34      A1
ATOM  380 CB  VAL  49     24.890  68.761  -9.636  1.00 44.29      A1
ATOM  381 CG1 VAL  49     23.381  68.709  -9.830  1.00 47.50      A1
ATOM  382 CG2 VAL  49     25.540  69.086 -10.975  1.00 45.25      A1
ATOM  383 C   VAL  49     24.740  71.214  -9.028  1.00 44.98      A1
ATOM  384 O   VAL  49     25.401  71.901  -9.814  1.00 46.03      A1
ATOM  385 N   LEU  50     23.565  71.602  -8.530  1.00 46.16      A1
ATOM  386 H   LEU  50     23.081  70.933  -8.006  1.00  0.00      A1
ATOM  387 CA  LEU  50     22.908  72.895  -8.729  1.00 46.03      A1
ATOM  388 CB  LEU  50     21.469  72.769  -8.264  1.00 46.43      A1
ATOM  389 CG  LEU  50     20.443  73.718  -8.760  1.00 44.16      A1
ATOM  390 CD1 LEU  50     20.259  73.558 -10.243  1.00 44.79      A1
ATOM  391 CD2 LEU  50     19.159  73.400  -8.079  1.00 44.66      A1
ATOM  392 C   LEU  50     23.632  73.968  -7.917  1.00 45.85      A1
ATOM  393 O   LEU  50     23.996  74.989  -8.484  1.00 44.52      A1
ATOM  394 N   LEU  51     23.853  73.764  -6.606  1.00 45.44      A1
ATOM  395 H   LEU  51     23.489  72.958  -6.189  1.00  0.00      A1
ATOM  396 CA  LEU  51     24.676  74.656  -5.805  1.00 46.04      A1
ATOM  397 CB  LEU  51     24.860  74.084  -4.435  1.00 45.58      A1
ATOM  398 CG  LEU  51     25.741  74.931  -3.535  1.00 47.78      A1
ATOM  399 CD1 LEU  51     25.148  76.320  -3.322  1.00 47.13      A1
ATOM  400 CD2 LEU  51     25.902  74.202  -2.219  1.00 48.33      A1
ATOM  401 C   LEU  51     26.064  74.845  -6.436  1.00 46.27      A1
ATOM  402 O   LEU  51     26.551  75.966  -6.612  1.00 47.62      A1
ATOM  403 N   GLY  52     26.702  73.736  -6.809  1.00 44.84      A1
ATOM  404 H   GLY  52     26.306  72.869  -6.578  1.00  0.00      A1
ATOM  405 CA  GLY  52     27.989  73.758  -7.453  1.00 42.91      A1
ATOM  406 C   GLY  52     27.984  74.533  -8.750  1.00 42.47      A1
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FIGURE 5

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ATOM  407 O   GLY  52     28.853  75.364  -8.983  1.00 42.06      A1
ATOM  408 N   HIS  53     27.047  74.307  -9.653  1.00 42.02      A1
ATOM  409 H   HIS  53     26.366  73.624  -9.471  1.00  0.00      A1
ATOM  410 CA  HIS  53     27.009  75.104 -10.861  1.00 42.23      A1
ATOM  411 CB  HIS  53     25.842  74.689 -11.706  1.00 42.21      A1
ATOM  412 CG  HIS  53     26.076  73.399 -12.460  1.00 44.60      A1
ATOM  413 CD2 HIS  53     25.112  72.774 -13.200  1.00 47.49      A1
ATOM  414 ND1 HIS  53     27.180  72.669 -12.578  1.00 46.76      A1
ATOM  415 HD1 HIS  53     28.039  72.853 -12.139  1.00  0.00      A1
ATOM  416 CE1 HIS  53     26.954  71.641 -13.346  1.00 46.90      A1
ATOM  417 NE2 HIS  53     25.704  71.725 -13.707  1.00 50.22      A1
ATOM  418 HE2 HIS  53     25.237  71.033 -14.239  1.00  0.00      A1
ATOM  419 C   HIS  53     26.893  76.585 -10.536  1.00 42.72      A1
ATOM  420 O   HIS  53     27.622  77.399 -11.068  1.00 42.03      A1
ATOM  421 N   SER  54     26.099  76.920  -9.535  1.00 45.08      A1
ATOM  422 H   SER  54     25.673  76.218  -9.001  1.00  0.00      A1
ATOM  423 CA  SER  54     25.792  78.278  -9.177  1.00 46.92      A1
ATOM  424 CB  SER  54     24.576  78.181  -8.289  1.00 48.86      A1
ATOM  425 OG  SER  54     23.521  77.616  -9.112  1.00 53.06      A1
ATOM  426 HG  SER  54     23.465  76.677  -8.918  1.00  0.00      A1
ATOM  427 C   SER  54     26.939  79.033  -8.549  1.00 47.92      A1
ATOM  428 O   SER  54     27.038  80.264  -8.655  1.00 49.60      A1
ATOM  429 N   LEU  55     27.837  78.273  -7.933  1.00 47.59      A1
ATOM  430 H   LEU  55     27.638  77.322  -7.791  1.00  0.00      A1
ATOM  431 CA  LEU  55     29.075  78.810  -7.401  1.00 45.27      A1
ATOM  432 CB  LEU  55     29.552  77.913  -6.243  1.00 45.49      A1
ATOM  433 CG  LEU  55     28.840  77.992  -4.874  1.00 47.30      A1
ATOM  434 CD1 LEU  55     28.876  76.596  -4.299  1.00 49.52      A1
ATOM  435 CD2 LEU  55     29.530  78.921  -3.862  1.00 45.69      A1
ATOM  436 C   LEU  55     30.133  78.889  -8.492  1.00 43.63      A1
ATOM  437 O   LEU  55     31.247  79.350  -8.272  1.00 43.24      A1
ATOM  438 N   GLY  56     29.855  78.383  -9.675  1.00 43.55      A1
ATOM  439 H   GLY  56     28.984  77.975  -9.828  1.00  0.00      A1
ATOM  440 CA  GLY  56     30.814  78.390 -10.753  1.00 45.59      A1
ATOM  441 C   GLY  56     32.182  77.811 -10.392  1.00 46.76      A1
ATOM  442 O   GLY  56     33.171  78.213 -11.015  1.00 47.31      A1
ATOM  443 N   ILE  57     32.247  76.885  -9.412  1.00 47.49      A1
ATOM  444 H   ILE  57     31.392  76.594  -9.042  1.00  0.00      A1
ATOM  445 CA  ILE  57     33.486  76.249  -8.950  1.00 48.28      A1
ATOM  446 CB  ILE  57     33.144  75.172  -7.863  1.00 47.79      A1
ATOM  447 CG2 ILE  57     34.457  74.591  -7.348  1.00 46.85      A1
ATOM  448 CG1 ILE  57     32.338  75.764  -6.701  1.00 45.09      A1
ATOM  449 CD  ILE  57     31.859  74.739  -5.659  1.00 41.23      A1
ATOM  450 C   ILE  57     34.276  75.602 -10.115  1.00 49.15      A1
ATOM  451 O   ILE  57     33.678  74.935 -10.968  1.00 49.04      A1
ATOM  452 N   PRO  58     35.596  75.817 -10.248  1.00 49.75      A1
ATOM  453 CD  PRO  58     36.402  76.743  -9.433  1.00 50.94      A1
ATOM  454 CA  PRO  58     36.421  75.228 -11.302  1.00 50.72      A1
ATOM  455 CB  PRO  58     37.525  76.241 -11.488  1.00 50.92      A1
ATOM  456 CG  PRO  58     37.814  76.663 -10.041  1.00 50.82      A1
ATOM  457 C   PRO  58     36.916  73.845 -10.875  1.00 50.36      A1
ATOM  458 O   PRO  58     37.187  73.599  -9.691  1.00 49.75      A1
ATOM  459 N   TRP  59     37.030  72.927 -11.816  1.00 50.37      A1
ATOM  460 H   TRP  59     36.888  73.141 -12.760  1.00  0.00      A1
ATOM  461 CA  TRP  59     37.524  71.595 -11.482  1.00 51.78      A1
ATOM  462 CB  TRP  59     36.435  70.562 -11.857  1.00 49.06      A1
ATOM  463 CG  TRP  59     35.254  70.712 -10.889  1.00 46.37      A1
ATOM  464 CD2 TRP  59     35.320  70.845  -9.521  1.00 44.06      A1
ATOM  465 CE2 TRP  59     33.998  71.027  -9.205  1.00 44.18      A1
ATOM  466 CE3 TRP  59     36.274  70.842  -8.538  1.00 44.03      A1
ATOM  467 CD1 TRP  59     33.972  70.794 -11.354  1.00 45.17      A1
ATOM  468 NE1 TRP  59     33.229  70.994 -10.297  1.00 45.17      A1
ATOM  469 HE1 TRP  59     32.301  71.312 -10.332  1.00  0.00      A1
ATOM  470 CZ2 TRP  59     33.598  71.215  -7.916  1.00 45.60      A1
ATOM  471 CZ3 TRP  59     35.893  71.028  -7.243  1.00 45.25      A1
ATOM  472 CH2 TRP  59     34.565  71.214  -6.938  1.00 46.43      A1
ATOM  473 C   TRP  59     38.815  71.435 -12.256  1.00 52.84      A1
ATOM  474 O   TRP  59     38.842  71.972 -13.372  1.00 54.96      A1
ATOM  475 N   ALA  60     39.912  70.834 -11.777  1.00 51.97      A1
ATOM  476 H   ALA  60     39.857  70.269 -10.977  1.00  0.00      A1
ATOM  477 CA  ALA  60     41.108  70.870 -12.609  1.00 52.18      A1
ATOM  478 CB  ALA  60     42.303  70.610 -11.748  1.00 51.75      A1
ATOM  479 C   ALA  60     41.055  69.857 -13.746  1.00 52.16      A1
ATOM  480 O   ALA  60     40.545  68.760 -13.530  1.00 52.17      A1
ATOM  481 N   PRO  61     41.435  70.145 -14.986  1.00 54.34      A1
ATOM  482 CD  PRO  61     41.370  71.458 -15.622  1.00 54.76      A1
ATOM  483 CA  PRO  61     41.691  69.145 -15.993  1.00 55.57      A1
ATOM  484 CB  PRO  61     41.792  69.918 -17.310  1.00 54.95      A1
ATOM  485 CG  PRO  61     42.211  71.297 -16.901  1.00 54.05      A1
ATOM  486 C   PRO  61     42.934  68.333 -15.690  1.00 57.54      A1
ATOM  487 O   PRO  61     43.757  68.661 -14.834  1.00 57.20      A1
ATOM  488 N   LEU  62     43.040  67.271 -16.486  1.00 59.98      A1
ATOM  489 H   LEU  62     42.285  67.067 -17.077  1.00  0.00      A1
ATOM  490 CA  LEU  62     44.184  66.370 -16.471  1.00 63.64      A1
ATOM  491 CB  LEU  62     44.062  65.417 -15.260  1.00 63.72      A1
ATOM  492 CG  LEU  62     45.323  64.691 -14.865  1.00 64.44      A1
ATOM  493 CD1 LEU  62     46.394  65.704 -14.488  1.00 64.02      A1
ATOM  494 CD2 LEU  62     45.016  63.764 -13.717  1.00 64.98      A1
ATOM  495 C   LEU  62     44.214  65.611 -17.812  1.00 65.69      A1
ATOM  496 OT1 LEU  62     44.256  66.302 -18.844  1.00 68.47      A1
ATOM  497 OT2 LEU  62     44.194  64.371 -17.845  1.00 66.57      A1
ATOM  498 CB  LEU  72     57.448  63.159 -19.422  1.00 63.44      A2
ATOM  499 CG  LEU  72     57.716  62.495 -18.117  1.00 63.40      A2
ATOM  500 CD1 LEU  72     56.719  61.408 -17.913  1.00 61.50      A2
ATOM  501 CD2 LEU  72     59.107  61.901 -18.121  1.00 63.22      A2
ATOM  502 C   LEU  72     55.897  65.084 -18.876  1.00 65.40      A2
ATOM  503 O   LEU  72     54.827  65.301 -18.316  1.00 67.80      A2
ATOM  504 HT1 LEU  72     56.469  64.683 -21.261  1.00  0.00      A2
ATOM  505 HT2 LEU  72     54.827  64.355 -20.951  1.00  0.00      A2
ATOM  506 N   LEU  72     55.795  63.983 -20.899  1.00 66.29      A2
ATOM  507 HT3 LEU  72     55.866  63.098 -21.419  1.00  0.00      A2
ATOM  508 CA  LEU  72     56.064  63.714 -19.512  1.00 64.91      A2
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FIGURE 5

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ATOM  509 N   ALA  73   56.807  66.046 -19.086  1.00 64.54    A2
ATOM  510 H   ALA  73   57.690  65.804 -19.432  1.00  0.00    A2
ATOM  511 CA  ALA  73   56.707  67.433 -18.615  1.00 62.55    A2
ATOM  512 CB  ALA  73   57.553  68.314 -19.529  1.00 64.84    A2
ATOM  513 C   ALA  73   55.319  68.024 -18.539  1.00 60.37    A2
ATOM  514 O   ALA  73   54.801  68.180 -17.456  1.00 59.42    A2
ATOM  515 N   GLY  74   54.693  68.226 -19.691  1.00 59.72    A2
ATOM  516 H   GLY  74   55.212  68.174 -20.514  1.00  0.00    A2
ATOM  517 CA  GLY  74   53.336  68.728 -19.816  1.00 59.99    A2
ATOM  518 C   GLY  74   52.327  68.114 -18.865  1.00 60.27    A2
ATOM  519 O   GLY  74   51.880  68.796 -17.935  1.00 60.80    A2
ATOM  520 N   CYS  75   51.945  66.850 -19.030  1.00 59.60    A2
ATOM  521 H   CYS  75   52.160  66.358 -19.839  1.00  0.00    A2
ATOM  522 CA  CYS  75   51.002  66.276 -18.078  1.00 60.17    A2
ATOM  523 CB  CYS  75   50.670  64.801 -18.464  1.00 64.08    A2
ATOM  524 SG  CYS  75   49.832  64.732 -20.096  1.00 73.47    A2
ATOM  525 C   CYS  75   51.502  66.346 -16.642  1.00 56.73    A2
ATOM  526 O   CYS  75   50.734  66.748 -15.765  1.00 55.82    A2
ATOM  527 N   LEU  76   52.795  66.142 -16.396  1.00 53.93    A2
ATOM  528 H   LEU  76   53.423  66.043 -17.137  1.00  0.00    A2
ATOM  529 CA  LEU  76   53.325  66.156 -15.044  1.00 52.94    A2
ATOM  530 CB  LEU  76   54.798  65.754 -15.181  1.00 50.81    A2
ATOM  531 CG  LEU  76   55.575  65.011 -14.090  1.00 49.02    A2
ATOM  532 CD1 LEU  76   54.852  63.740 -13.698  1.00 46.76    A2
ATOM  533 CD2 LEU  76   56.951  64.633 -14.623  1.00 47.67    A2
ATOM  534 C   LEU  76   53.093  67.545 -14.425  1.00 53.65    A2
ATOM  535 O   LEU  76   52.731  67.716 -13.244  1.00 53.50    A2
ATOM  536 N   SER  77   53.137  68.553 -15.301  1.00 53.91    A2
ATOM  537 H   SER  77   53.322  68.361 -16.242  1.00  0.00    A2
ATOM  538 CA  SER  77   52.882  69.932 -14.942  1.00 54.93    A2
ATOM  539 CB  SER  77   53.425  70.835 -16.040  1.00 58.32    A2
ATOM  540 OG  SER  77   54.806  70.587 -16.310  1.00 63.35    A2
ATOM  541 HG  SER  77   54.949  69.637 -16.315  1.00  0.00    A2
ATOM  542 C   SER  77   51.382  70.172 -14.759  1.00 53.47    A2
ATOM  543 O   SER  77   50.982  70.965 -13.899  1.00 53.54    A2
ATOM  544 N   GLN  78   50.509  69.501 -15.512  1.00 51.82    A2
ATOM  545 H   GLN  78   50.857  68.901 -16.207  1.00  0.00    A2
ATOM  546 CA  GLN  78   49.074  69.619 -15.349  1.00 50.74    A2
ATOM  547 CB  GLN  78   48.402  68.877 -16.451  1.00 54.31    A2
ATOM  548 CG  GLN  78   47.420  69.784 -17.160  1.00 58.59    A2
ATOM  549 CD  GLN  78   46.557  68.940 -18.071  1.00 62.32    A2
ATOM  550 OE1 GLN  78   47.005  68.260 -18.998  1.00 65.94    A2
ATOM  551 NE2 GLN  78   45.269  68.889 -17.800  1.00 63.17    A2
ATOM  552 HE21 GLN  78   44.973  69.327 -16.972  1.00  0.00    A2
ATOM  553 HE22 GLN  78   44.704  68.444 -18.456  1.00  0.00    A2
ATOM  554 C   GLN  78   48.591  69.065 -14.011  1.00 48.17    A2
ATOM  555 O   GLN  78   47.691  69.618 -13.368  1.00 46.31    A2
ATOM  556 N   LEU  79   49.236  67.988 -13.564  1.00 45.89    A2
ATOM  557 H   LEU  79   49.920  67.584 -14.140  1.00  0.00    A2
ATOM  558 CA  LEU  79   48.919  67.359 -12.294  1.00 44.54    A2
ATOM  559 CB  LEU  79   49.617  66.015 -12.259  1.00 45.06    A2
ATOM  560 CG  LEU  79   49.154  64.895 -11.351  1.00 45.18    A2
ATOM  561 CD1 LEU  79   49.634  63.594 -11.957  1.00 48.06    A2
ATOM  562 CD2 LEU  79   49.766  64.986 -9.969  1.00 46.03    A2
ATOM  563 C   LEU  79   49.366  68.265 -11.170  1.00 43.49    A2
ATOM  564 O   LEU  79   48.645  68.509 -10.199  1.00 43.20    A2
ATOM  565 N   HIS  80   50.556  68.834 -11.329  1.00 43.83    A2
ATOM  566 H   HIS  80   51.115  68.548 -12.085  1.00  0.00    A2
ATOM  567 CA  HIS  80   51.060  69.788 -10.360  1.00 43.79    A2
ATOM  568 CB  HIS  80   52.456  70.221 -10.810  1.00 43.58    A2
ATOM  569 CG  HIS  80   53.030  71.031 -9.690  1.00 43.75    A2
ATOM  570 CD2 HIS  80   53.484  70.497 -8.517  1.00 47.48    A2
ATOM  571 ND1 HIS  80   53.083  72.343 -9.567  1.00 44.24    A2
ATOM  572 HD1 HIS  80   52.842  73.004 -10.255  1.00  0.00    A2
ATOM  573 CE1 HIS  80   53.530  72.641 -8.376  1.00 44.47    A2
ATOM  574 NE2 HIS  80   53.772  71.520 -7.748  1.00 48.16    A2
ATOM  575 HE2 HIS  80   54.103  71.444 -6.824  1.00  0.00    A2
ATOM  576 C   HIS  80   50.094  70.978 -10.229  1.00 44.40    A2
ATOM  577 O   HIS  80   49.643  71.294 -9.131  1.00 44.28    A2
ATOM  578 N   SER  81   49.733  71.670 -11.309  1.00 45.13    A2
ATOM  579 H   SER  81   50.136  71.459 -12.176  1.00  0.00    A2
ATOM  580 CA  SER  81   48.738  72.742 -11.296  1.00 45.41    A2
ATOM  581 CB  SER  81   48.612  73.347 -12.682  1.00 45.59    A2
ATOM  582 OG  SER  81   49.894  73.444 -13.292  1.00 49.27    A2
ATOM  583 HG  SER  81   50.058  72.670 -13.843  1.00  0.00    A2
ATOM  584 C   SER  81   47.344  72.266 -10.856  1.00 44.85    A2
ATOM  585 O   SER  81   46.604  73.064 -10.256  1.00 46.93    A2
ATOM  586 N   GLY  82   46.946  71.010 -11.092  1.00 42.16    A2
ATOM  587 H   GLY  82   47.513  70.411 -11.614  1.00  0.00    A2
ATOM  588 CA  GLY  82   45.663  70.500 -10.650  1.00 39.49    A2
ATOM  589 C   GLY  82   45.569  70.461 -9.139  1.00 39.80    A2
ATOM  590 O   GLY  82   44.542  70.843 -8.544  1.00 39.64    A2
ATOM  591 N   LEU  83   46.676  70.032 -8.521  1.00 37.57    A2
ATOM  592 H   LEU  83   47.413  69.695 -9.075  1.00  0.00    A2
ATOM  593 CA  LEU  83   46.826  70.007 -7.057  1.00 38.07    A2
ATOM  594 CB  LEU  83   46.133  69.202 -6.748  1.00 35.67    A2
ATOM  595 CG  LEU  83   48.071  67.736 -7.275  1.00 32.51    A2
ATOM  596 CD1 LEU  83   49.442  67.145 -7.319  1.00 29.77    A2
ATOM  597 CD2 LEU  83   47.180  66.973 -6.288  1.00 28.71    A2
ATOM  598 C   LEU  83   46.836  71.386 -6.354  1.00 38.48    A2
ATOM  599 O   LEU  83   46.392  71.627 -5.219  1.00 38.05    A2
ATOM  600 N   PHE  84   47.366  72.338 -7.108  1.00 40.34    A2
ATOM  601 H   PHE  84   47.804  72.078 -7.944  1.00  0.00    A2
ATOM  602 CA  PHE  84   47.414  73.703 -6.688  1.00 41.54    A2
ATOM  603 CB  PHE  84   48.163  74.531 -7.693  1.00 46.88    A2
ATOM  604 CG  PHE  84   48.715  75.777 -6.988  1.00 55.09    A2
ATOM  605 CD1 PHE  84   49.521  75.622 -5.849  1.00 55.81    A2
ATOM  606 CD2 PHE  84   48.396  77.053 -7.469  1.00 55.79    A2
ATOM  607 CE1 PHE  84   50.004  76.737 -5.195  1.00 57.60    A2
ATOM  608 CE2 PHE  84   48.892  78.156 -6.796  1.00 57.25    A2
ATOM  609 CZ  PHE  84   49.688  78.002 -5.667  1.00 58.34    A2
ATOM  610 C   PHE  84   45.994  74.191 -6.501  1.00 40.47    A2
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FIGURE 5

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ATOM  611 O   PHE  84    45.609  74.749  -5.558  1.00 42.71      A2
ATOM  612 N   LEU  85    45.190  73.953  -7.624  1.00 38.64      A2
ATOM  613 H   LEU  85    45.555  73.527  -8.429  1.00  0.00      A2
ATOM  614 CA  LEU  85    43.794  74.335  -7.584  1.00 38.81      A2
ATOM  615 CB  LEU  85    43.101  73.886  -8.839  1.00 41.27      A2
ATOM  616 CG  LEU  85    41.673  74.403  -9.017  1.00 46.45      A2
ATOM  617 CD1 LEU  85    41.702  75.784  -9.719  1.00 47.80      A2
ATOM  618 CD2 LEU  85    40.860  73.359  -9.787  1.00 48.25      A2
ATOM  619 C   LEU  85    43.079  73.731  -6.386  1.00 38.20      A2
ATOM  620 O   LEU  85    42.498  74.469  -5.582  1.00 38.36      A2
ATOM  621 N   TYR  86    43.150  72.405  -6.198  1.00 37.92      A2
ATOM  622 H   TYR  86    43.637  71.850  -6.845  1.00  0.00      A2
ATOM  623 CA  TYR  86    42.501  71.801  -5.057  1.00 37.15      A2
ATOM  624 CB  TYR  86    42.598  70.255  -5.102  1.00 36.73      A2
ATOM  625 CG  TYR  86    41.561  69.685  -6.081  1.00 33.66      A2
ATOM  626 CD1 TYR  86    41.946  69.312  -7.374  1.00 30.03      A2
ATOM  627 CE1 TYR  86    40.991  68.885  -8.280  1.00 30.08      A2
ATOM  628 CD2 TYR  86    40.224  69.623  -5.666  1.00 32.61      A2
ATOM  629 CE2 TYR  86    39.263  69.203  -6.574  1.00 31.66      A2
ATOM  630 CZ  TYR  86    39.656  68.838  -7.868  1.00 30.57      A2
ATOM  631 OH  TYR  86    38.670  68.428  -8.751  1.00 28.18      A2
ATOM  632 HH  TYR  86    39.107  67.994  -9.485  1.00  0.00      A2
ATOM  633 C   TYR  86    43.054  72.318  -3.746  1.00 37.75      A2
ATOM  634 O   TYR  86    42.173  72.469  -2.889  1.00 39.52      A2
ATOM  635 N   GLN  87    44.347  72.655  -3.478  1.00 36.93      A2
ATOM  636 H   GLN  87    45.044  72.463  -4.140  1.00  0.00      A2
ATOM  637 CA  GLN  87    44.749  73.332  -2.205  1.00 36.40      A2
ATOM  638 CB  GLN  87    46.210  73.668  -2.255  1.00 39.56      A2
ATOM  639 CG  GLN  87    47.126  72.993  -1.237  1.00 46.99      A2
ATOM  640 CD  GLN  87    48.641  73.062  -1.576  1.00 50.96      A2
ATOM  641 OE1 GLN  87    49.144  72.623  -2.627  1.00 52.15      A2
ATOM  642 NE2 GLN  87    49.446  73.608  -0.663  1.00 52.96      A2
ATOM  643 HE21 GLN  87    49.055  73.957   0.164  1.00  0.00      A2
ATOM  644 HE22 GLN  87    50.396  73.621  -0.888  1.00  0.00      A2
ATOM  645 C   GLN  87    43.941  74.652  -2.013  1.00 34.36      A2
ATOM  646 O   GLN  87    43.414  74.990  -0.935  1.00 31.55      A2
ATOM  647 N   GLY  88    43.740  75.335  -3.159  1.00 32.73      A2
ATOM  648 H   GLY  88    44.165  75.005  -3.981  1.00  0.00      A2
ATOM  649 CA  GLY  88    42.948  76.546  -3.232  1.00 30.81      A2
ATOM  650 C   GLY  88    41.540  76.275  -2.731  1.00 30.47      A2
ATOM  651 O   GLY  88    41.130  76.819  -1.703  1.00 30.27      A2
ATOM  652 N   LEU  89    40.802  75.387  -3.406  1.00 29.01      A2
ATOM  653 H   LEU  89    41.220  74.912  -4.154  1.00  0.00      A2
ATOM  654 CA  LEU  89    39.447  75.102  -3.009  1.00 27.60      A2
ATOM  655 CB  LEU  89    38.922  74.073  -3.935  1.00 28.13      A2
ATOM  656 CG  LEU  89    38.764  74.583  -5.340  1.00 29.51      A2
ATOM  657 CD1 LEU  89    38.363  73.530  -6.364  1.00 24.13      A2
ATOM  658 CD2 LEU  89    37.673  75.637  -5.220  1.00 32.87      A2
ATOM  659 C   LEU  89    39.352  74.629  -1.583  1.00 29.88      A2
ATOM  660 O   LEU  89    38.427  75.012  -0.860  1.00 30.81      A2
ATOM  661 N   LEU  90    40.317  73.839  -1.094  1.00 32.59      A2
ATOM  662 H   LEU  90    41.101  73.626  -1.643  1.00  0.00      A2
ATOM  663 CA  LEU  90    40.182  73.274   0.235  1.00 33.41      A2
ATOM  664 CB  LEU  90    41.207  72.234   0.503  1.00 36.15      A2
ATOM  665 CG  LEU  90    41.075  70.971  -0.343  1.00 38.76      A2
ATOM  666 CD1 LEU  90    42.431  70.267  -0.456  1.00 37.21      A2
ATOM  667 CD2 LEU  90    39.995  70.099   0.279  1.00 40.54      A2
ATOM  668 C   LEU  90    40.342  74.319   1.255  1.00 34.24      A2
ATOM  669 O   LEU  90    39.711  74.256   2.313  1.00 35.57      A2
ATOM  670 N   GLN  91    41.188  75.291   0.940  1.00 35.24      A2
ATOM  671 H   GLN  91    41.663  75.284   0.078  1.00  0.00      A2
ATOM  672 CA  GLN  91    41.397  76.373   1.883  1.00 37.60      A2
ATOM  673 CB  GLN  91    42.557  77.182   1.363  1.00 39.65      A2
ATOM  674 CG  GLN  91    43.155  78.237   2.284  1.00 44.37      A2
ATOM  675 CD  GLN  91    44.348  78.799   1.542  1.00 46.96      A2
ATOM  676 OE1 GLN  91    45.235  78.083   1.068  1.00 47.42      A2
ATOM  677 NE2 GLN  91    44.376  80.092   1.341  1.00 46.82      A2
ATOM  678 HE21 GLN  91    43.690  80.685   1.700  1.00  0.00      A2
ATOM  679 HE22 GLN  91    45.108  80.331   0.741  1.00  0.00      A2
ATOM  680 C   GLN  91    40.129  77.231   2.061  1.00 37.22      A2
ATOM  681 O   GLN  91    39.718  77.530   3.186  1.00 36.21      A2
ATOM  682 N   ALA  92    39.456  77.570   0.943  1.00 38.63      A2
ATOM  683 H   ALA  92    39.808  77.205   0.098  1.00  0.00      A2
ATOM  684 CA  ALA  92    38.243  78.402   0.880  1.00 38.10      A2
ATOM  685 CB  ALA  92    37.657  78.436  -0.511  1.00 36.76      A2
ATOM  686 C   ALA  92    37.139  77.905   1.770  1.00 38.95      A2
ATOM  687 O   ALA  92    36.294  78.687   2.194  1.00 42.45      A2
ATOM  688 N   LEU  93    37.151  76.618   2.123  1.00 38.34      A2
ATOM  689 H   LEU  93    37.855  76.040   1.759  1.00  0.00      A2
ATOM  690 CA  LEU  93    36.111  76.018   2.972  1.00 36.90      A2
ATOM  691 CB  LEU  93    36.088  74.463   2.794  1.00 35.24      A2
ATOM  692 CG  LEU  93    35.725  73.992   1.378  1.00 33.55      A2
ATOM  693 CD1 LEU  93    36.159  72.583   1.129  1.00 33.26      A2
ATOM  694 CD2 LEU  93    34.254  74.167   1.215  1.00 32.18      A2
ATOM  695 C   LEU  93    36.264  76.353   4.426  1.00 36.44      A2
ATOM  696 O   LEU  93    35.473  75.917   5.256  1.00 35.17      A2
ATOM  697 N   GLU  94    37.357  77.019   4.736  1.00 38.19      A2
ATOM  698 H   GLU  94    38.022  77.167   4.035  1.00  0.00      A2
ATOM  699 CA  GLU  94    37.627  77.573   6.038  1.00 42.71      A2
ATOM  700 CB  GLU  94    36.931  78.947   6.165  1.00 47.48      A2
ATOM  701 CG  GLU  94    37.418  80.011   5.131  1.00 56.10      A2
ATOM  702 CD  GLU  94    36.423  81.153   4.862  1.00 60.26      A2
ATOM  703 OE1 GLU  94    35.728  81.109   3.823  1.00 60.76      A2
ATOM  704 OE2 GLU  94    36.331  82.054   5.721  1.00 61.64      A2
ATOM  705 C   GLU  94    37.245  76.701   7.198  1.00 43.90      A2
ATOM  706 O   GLU  94    36.624  77.172   8.167  1.00 45.70      A2
ATOM  707 N   GLY  95    37.641  75.410   7.001  1.00 44.03      A2
ATOM  708 H   GLY  95    38.024  75.192   6.127  1.00  0.00      A2
ATOM  709 CA  GLY  95    37.519  74.310   7.981  1.00 42.49      A2
ATOM  710 C   GLY  95    36.162  73.612   8.061  1.00 42.24      A2
ATOM  711 O   GLY  95    36.028  72.596   8.759  1.00 40.02      A2
ATOM  712 N   ILE  96    35.160  74.123   7.328  1.00 42.82      A2
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FIGURE 5

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ATOM  713 H   ILE  96    35.357 74.944  6.841 1.00 0.00    A2
ATOM  714 CA  ILE  96    33.760 73.692  7.312 1.00 42.12   A2
ATOM  715 CB  ILE  96    33.665 72.233  6.800 1.00 36.33   A2
ATOM  716 CG2 ILE  96    32.248 71.768  6.789 1.00 34.79   A2
ATOM  717 CG1 ILE  96    34.091 72.157  5.374 1.00 35.35   A2
ATOM  718 CD  ILE  96    34.051 70.743  4.738 1.00 33.64   A2
ATOM  719 C   ILE  96    33.106 73.863  8.709 1.00 44.74   A2
ATOM  720 O   ILE  96    32.220 74.716  8.841 1.00 44.59   A2
ATOM  721 N   SER  97    33.467 73.154  9.780 1.00 46.84   A2
ATOM  722 H   SER  97    34.243 72.553  9.706 1.00 0.00    A2
ATOM  723 CA  SER  97    32.900 73.359 11.105 1.00 48.91   A2
ATOM  724 CB  SER  97    31.804 72.343 11.347 1.00 49.60   A2
ATOM  725 OG  SER  97    32.211 71.120 11.954 1.00 52.85   A2
ATOM  726 HG  SER  97    31.406 70.573 11.942 1.00 0.00    A2
ATOM  727 C   SER  97    34.045 73.143 12.077 1.00 50.64   A2
ATOM  728 O   SER  97    35.035 72.538 11.678 1.00 52.78   A2
ATOM  729 N   PRO  98    34.063 73.474 13.348 1.00 52.12   A2
ATOM  730 CD  PRO  98    33.002 74.170 14.016 1.00 52.90   A2
ATOM  731 CA  PRO  98    35.195 73.200 14.257 1.00 54.94   A2
ATOM  732 CB  PRO  98    34.750 73.717 15.600 1.00 54.78   A2
ATOM  733 CG  PRO  98    33.772 74.777 15.182 1.00 55.48   A2
ATOM  734 C   PRO  98    35.591 71.723 14.336 1.00 56.75   A2
ATOM  735 O   PRO  98    36.738 71.274 14.468 1.00 57.85   A2
ATOM  736 N   GLU  99    34.509 70.971 14.214 1.00 58.21   A2
ATOM  737 H   GLU  99    33.652 71.400 14.028 1.00 0.00    A2
ATOM  738 CA  GLU  99    34.543 69.537 14.281 1.00 58.48   A2
ATOM  739 CB  GLU  99    33.111 69.104 14.304 1.00 63.30   A2
ATOM  740 CG  GLU  99    32.958 67.702 14.852 1.00 71.04   A2
ATOM  741 CD  GLU  99    32.076 66.838 13.962 1.00 76.95   A2
ATOM  742 OE1 GLU  99    32.209 65.608 14.079 1.00 80.63   A2
ATOM  743 OE2 GLU  99    31.295 67.382 13.153 1.00 77.99   A2
ATOM  744 C   GLU  99    35.298 69.025 13.074 1.00 55.31   A2
ATOM  745 O   GLU  99    36.251 68.270 13.210 1.00 55.96   A2
ATOM  746 N   LEU 100    34.916 69.475 11.891 1.00 51.23   A2
ATOM  747 H   LEU 100    34.214 70.159 11.841 1.00 0.00    A2
ATOM  748 CA  LEU 100    35.577 69.052 10.678 1.00 48.08   A2
ATOM  749 CB  LEU 100    34.627 69.341  9.574 1.00 45.52   A2
ATOM  750 CG  LEU 100    33.544 68.337  9.674 1.00 45.39   A2
ATOM  751 CD1 LEU 100    32.207 68.972  9.458 1.00 46.40   A2
ATOM  752 CD2 LEU 100    33.851 67.245  8.677 1.00 47.48   A2
ATOM  753 C   LEU 100    36.956 69.629 10.368 1.00 46.77   A2
ATOM  754 O   LEU 100    37.578 69.244  9.357 1.00 46.62   A2
ATOM  755 N   GLY 101    37.441 70.505 11.272 1.00 45.40   A2
ATOM  756 H   GLY 101    36.893 70.704 12.056 1.00 0.00    A2
ATOM  757 CA  GLY 101    38.703 71.238 11.126 1.00 42.52   A2
ATOM  758 C   GLY 101    39.885 70.334 10.798 1.00 40.73   A2
ATOM  759 O   GLY 101    40.475 70.402  9.710 1.00 40.69   A2
ATOM  760 N   PRO 102    40.250 69.441 11.708 1.00 38.61   A2
ATOM  761 CD  PRO 102    39.676 69.350 13.027 1.00 39.26   A2
ATOM  762 CA  PRO 102    41.390 68.566 11.606 1.00 37.30   A2
ATOM  763 CB  PRO 102    41.294 67.690 12.775 1.00 39.36   A2
ATOM  764 CG  PRO 102    40.799 68.687 13.776 1.00 41.02   A2
ATOM  765 C   PRO 102    41.364 67.795 10.331 1.00 37.15   A2
ATOM  766 O   PRO 102    42.358 67.854  9.600 1.00 38.88   A2
ATOM  767 N   THR 103    40.223 67.167 10.045 1.00 35.36   A2
ATOM  768 H   THR 103    39.466 67.223 10.662 1.00 0.00    A2
ATOM  769 CA  THR 103    40.051 66.386  8.843 1.00 34.02   A2
ATOM  770 CB  THR 103    38.592 65.888  8.715 1.00 34.07   A2
ATOM  771 OG1 THR 103    38.356 65.240  9.936 1.00 35.43   A2
ATOM  772 HG1 THR 103    38.011 65.896 10.548 1.00 0.00    A2
ATOM  773 CG2 THR 103    38.312 64.896  7.594 1.00 31.29   A2
ATOM  774 C   THR 103    40.417 67.215  7.625 1.00 34.61   A2
ATOM  775 O   THR 103    41.091 66.665  6.738 1.00 38.16   A2
ATOM  776 N   LEU 104    40.054 68.498  7.529 1.00 32.49   A2
ATOM  777 H   LEU 104    39.504 68.923  8.229 1.00 0.00    A2
ATOM  778 CA  LEU 104    40.471 69.267  6.370 1.00 30.49   A2
ATOM  779 CB  LEU 104    39.616 70.430  6.242 1.00 33.51   A2
ATOM  780 CG  LEU 104    38.356 69.996  5.611 1.00 36.61   A2
ATOM  781 CD1 LEU 104    37.222 70.621  6.381 1.00 39.43   A2
ATOM  782 CD2 LEU 104    38.418 70.294  4.132 1.00 37.69   A2
ATOM  783 C   LEU 104    41.904 69.727  6.414 1.00 28.48   A2
ATOM  784 O   LEU 104    42.583 69.825  5.398 1.00 28.47   A2
ATOM  785 N   ASP 105    42.449 69.949  7.574 1.00 26.99   A2
ATOM  786 H   ASP 105    41.903 69.912  8.388 1.00 0.00    A2
ATOM  787 CA  ASP 105    43.822 70.307  7.613 1.00 28.67   A2
ATOM  788 CB  ASP 105    44.139 70.584  9.038 1.00 33.06   A2
ATOM  789 CG  ASP 105    43.438 71.808  9.593 1.00 35.46   A2
ATOM  790 OD1 ASP 105    43.085 72.726  8.836 1.00 38.42   A2
ATOM  791 OD2 ASP 105    43.244 71.816 10.808 1.00 39.10   A2
ATOM  792 C   ASP 105    44.701 69.206  7.032 1.00 28.90   A2
ATOM  793 O   ASP 105    45.551 69.479  6.175 1.00 29.62   A2
ATOM  794 N   THR 106    44.415 67.950  7.401 1.00 26.86   A2
ATOM  795 H   THR 106    43.674 67.826  8.029 1.00 0.00    A2
ATOM  796 CA  THR 106    45.143 66.770  6.935 1.00 24.81   A2
ATOM  797 CB  THR 106    44.558 65.456  7.477 1.00 26.03   A2
ATOM  798 OG1 THR 106    44.680 65.566  8.894 1.00 31.53   A2
ATOM  799 HG1 THR 106    44.069 66.223  9.242 1.00 0.00    A2
ATOM  800 CG2 THR 106    45.258 64.220  7.011 1.00 20.90   A2
ATOM  801 C   THR 106    45.073 66.684  5.460 1.00 23.75   A2
ATOM  802 O   THR 106    46.065 66.411  4.812 1.00 24.68   A2
ATOM  803 N   LEU 107    43.887 66.917  4.946 1.00 24.30   A2
ATOM  804 H   LEU 107    43.145 67.176  5.528 1.00 0.00    A2
ATOM  805 CA  LEU 107    43.668 66.783  3.531 1.00 27.29   A2
ATOM  806 CB  LEU 107    42.158 66.913  3.273 1.00 25.45   A2
ATOM  807 CG  LEU 107    41.642 66.888  1.863 1.00 26.24   A2
ATOM  808 CD1 LEU 107    42.095 65.649  1.158 1.00 26.41   A2
ATOM  809 CD2 LEU 107    40.140 66.925  1.914 1.00 27.62   A2
ATOM  810 C   LEU 107    44.485 67.848  2.819 1.00 28.01   A2
ATOM  811 O   LEU 107    45.154 67.555  1.823 1.00 30.72   A2
ATOM  812 N   GLN 108    44.540 69.055  3.373 1.00 28.52   A2
ATOM  813 H   GLN 108    44.030 69.221  4.194 1.00 0.00    A2
ATOM  814 CA  GLN 108    45.343 70.132  2.792 1.00 28.38   A2
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FIGURE 5

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ATOM  815 CB  GLN  108      45.138  71.363   3.630  1.00 30.15      A2
ATOM  816 CG  GLN  108      43.711  71.787   3.542  1.00 32.67      A2
ATOM  817 CD  GLN  108      43.606  73.192   4.048  1.00 35.24      A2
ATOM  818 OE1 GLN  108      43.085  73.484   5.125  1.00 36.07      A2
ATOM  819 NE2 GLN  108      44.189  74.044   3.213  1.00 33.58      A2
ATOM  820 HE21 GLN  108     44.582  73.701   2.386  1.00  0.00      A2
ATOM  821 HE22 GLN  108     44.195  74.986   3.471  1.00  0.00      A2
ATOM  822 C   GLN  108      46.840  69.842   2.675  1.00 26.40      A2
ATOM  823 O   GLN  108      47.450  69.955   1.597  1.00 27.57      A2
ATOM  824 N   LEU  109      47.388  69.473   3.833  1.00 25.81      A2
ATOM  825 H   LEU  109      46.795  69.495   4.615  1.00  0.00      A2
ATOM  826 CA  LEU  109      48.764  69.003   4.043  1.00 27.96      A2
ATOM  827 CB  LEU  109      48.951  68.637   5.513  1.00 29.41      A2
ATOM  828 CG  LEU  109      48.712  69.771   6.520  1.00 31.78      A2
ATOM  829 CD1 LEU  109      48.750  69.188   7.933  1.00 29.16      A2
ATOM  830 CD2 LEU  109      49.724  70.889   6.285  1.00 32.19      A2
ATOM  831 C   LEU  109      49.168  67.790   3.186  1.00 26.80      A2
ATOM  832 O   LEU  109      50.214  67.721   2.544  1.00 26.81      A2
ATOM  833 N   ASP  110      48.305  66.807   3.090  1.00 25.98      A2
ATOM  834 H   ASP  110      47.471  66.835   3.600  1.00  0.00      A2
ATOM  835 CA  ASP  110      48.590  65.684   2.250  1.00 23.32      A2
ATOM  836 CB  ASP  110      47.577  64.570   2.553  1.00 26.34      A2
ATOM  837 CG  ASP  110      47.905  63.878   3.894  1.00 31.10      A2
ATOM  838 OD1 ASP  110      47.070  63.093   4.323  1.00 34.98      A2
ATOM  839 OD2 ASP  110      48.958  64.107   4.535  1.00 34.06      A2
ATOM  840 C   ASP  110      48.557  66.138   0.842  1.00 21.31      A2
ATOM  841 O   ASP  110      49.493  65.711   0.165  1.00 20.63      A2
ATOM  842 N   VAL  111      47.627  66.998   0.363  1.00 20.80      A2
ATOM  843 H   VAL  111      46.900  67.310   0.944  1.00  0.00      A2
ATOM  844 CA  VAL  111      47.711  67.454  -1.019  1.00 20.44      A2
ATOM  845 CB  VAL  111      46.531  68.364  -1.376  1.00 23.60      A2
ATOM  846 CG1 VAL  111      46.615  68.946  -2.808  1.00 23.04      A2
ATOM  847 CG2 VAL  111      45.289  67.497  -1.371  1.00 24.30      A2
ATOM  848 C   VAL  111      49.006  68.224  -1.245  1.00 20.82      A2
ATOM  849 O   VAL  111      49.617  68.006  -2.303  1.00 19.22      A2
ATOM  850 N   ALA  112      49.442  69.063  -0.267  1.00 21.84      A2
ATOM  851 H   ALA  112      48.839  69.190   0.492  1.00  0.00      A2
ATOM  852 CA  ALA  112      50.708  69.805  -0.295  1.00 24.16      A2
ATOM  853 CB  ALA  112      50.861  70.561   1.011  1.00 22.69      A2
ATOM  854 C   ALA  112      51.931  68.878  -0.486  1.00 28.58      A2
ATOM  855 O   ALA  112      52.778  69.026  -1.390  1.00 32.53      A2
ATOM  856 N   ASP  113      52.086  67.852   0.343  1.00 30.21      A2
ATOM  857 H   ASP  113      51.507  67.817   1.130  1.00  0.00      A2
ATOM  858 CA  ASP  113      53.084  66.846   0.166  1.00 31.70      A2
ATOM  859 CB  ASP  113      52.706  65.659   0.953  1.00 36.31      A2
ATOM  860 CG  ASP  113      53.170  65.758   2.357  1.00 42.27      A2
ATOM  861 OD1 ASP  113      52.559  65.109   3.203  1.00 46.37      A2
ATOM  862 OD2 ASP  113      54.160  66.461   2.589  1.00 48.93      A2
ATOM  863 C   ASP  113      53.315  66.361  -1.239  1.00 32.82      A2
ATOM  864 O   ASP  113      54.433  66.308  -1.754  1.00 36.25      A2
ATOM  865 N   PHE  114      52.187  65.978  -1.830  1.00 30.94      A2
ATOM  866 H   PHE  114      51.344  66.164  -1.361  1.00  0.00      A2
ATOM  867 CA  PHE  114      52.109  65.328  -3.103  1.00 27.84      A2
ATOM  868 CB  PHE  114      50.708  64.794  -3.226  1.00 23.18      A2
ATOM  869 CG  PHE  114      50.565  63.928  -4.420  1.00 21.04      A2
ATOM  870 CD1 PHE  114      51.623  63.225  -4.938  1.00 24.05      A2
ATOM  871 CD2 PHE  114      49.369  63.914  -5.046  1.00 22.37      A2
ATOM  872 CE1 PHE  114      51.476  62.514  -6.102  1.00 24.54      A2
ATOM  873 CE2 PHE  114      49.211  63.207  -6.212  1.00 21.33      A2
ATOM  874 CZ  PHE  114      50.263  62.509  -6.741  1.00 24.71      A2
ATOM  875 C   PHE  114      52.453  66.291  -4.190  1.00 29.20      A2
ATOM  876 O   PHE  114      53.072  65.883  -5.158  1.00 30.84      A2
ATOM  877 N   ALA  115      52.057  67.554  -4.058  1.00 31.99      A2
ATOM  878 H   ALA  115      51.446  67.768  -3.317  1.00  0.00      A2
ATOM  879 CA  ALA  115      52.423  68.655  -4.952  1.00 31.29      A2
ATOM  880 CB  ALA  115      51.824  69.939  -4.420  1.00 30.65      A2
ATOM  881 C   ALA  115      53.936  68.787  -4.976  1.00 31.31      A2
ATOM  882 O   ALA  115      54.539  68.823  -6.044  1.00 30.36      A2
ATOM  883 N   THR  116      54.551  68.846  -3.813  1.00 32.20      A2
ATOM  884 H   THR  116      54.013  68.910  -2.992  1.00  0.00      A2
ATOM  885 CA  THR  116      55.998  68.897  -3.656  1.00 34.91      A2
ATOM  886 CB  THR  116      56.325  68.953  -2.150  1.00 35.78      A2
ATOM  887 OG1 THR  116      55.564  70.038  -1.576  1.00 35.58      A2
ATOM  888 HG1 THR  116      54.942  69.644  -0.939  1.00  0.00      A2
ATOM  889 CG2 THR  116      57.816  69.050  -1.921  1.00 35.38      A2
ATOM  890 C   THR  116      56.714  67.726  -4.304  1.00 37.14      A2
ATOM  891 O   THR  116      57.641  67.937  -5.066  1.00 39.27      A2
ATOM  892 N   THR  117      56.318  66.485  -4.045  1.00 39.05      A2
ATOM  893 H   THR  117      55.615  66.383  -3.369  1.00  0.00      A2
ATOM  894 CA  THR  117      56.840  65.269  -4.630  1.00 40.23      A2
ATOM  895 CB  THR  117      55.909  64.090  -4.216  1.00 39.99      A2
ATOM  896 OG1 THR  117      56.149  63.920  -2.820  1.00 41.66      A2
ATOM  897 HG1 THR  117      55.653  64.559  -2.286  1.00  0.00      A2
ATOM  898 CG2 THR  117      56.110  62.781  -4.981  1.00 38.23      A2
ATOM  899 C   THR  117      56.882  65.417  -6.134  1.00 43.42      A2
ATOM  900 O   THR  117      57.934  65.253  -6.749  1.00 46.29      A2
ATOM  901 N   ILE  118      55.763  65.777  -6.741  1.00 45.87      A2
ATOM  902 H   ILE  118      54.962  65.942  -6.200  1.00  0.00      A2
ATOM  903 CA  ILE  118      55.659  65.914  -8.182  1.00 47.97      A2
ATOM  904 CB  ILE  118      54.170  66.271  -8.452  1.00 47.69      A2
ATOM  905 CG2 ILE  118      54.041  66.930  -9.835  1.00 47.04      A2
ATOM  906 CG1 ILE  118      53.302  65.011  -8.244  1.00 44.00      A2
ATOM  907 CD  ILE  118      53.651  63.883  -9.236  1.00 43.71      A2
ATOM  908 C   ILE  118      56.647  66.932  -8.724  1.00 50.69      A2
ATOM  909 O   ILE  118      57.390  66.676  -9.681  1.00 49.98      A2
ATOM  910 N   TRP  119      56.697  68.061  -8.015  1.00 54.68      A2
ATOM  911 H   TRP  119      56.164  68.135  -7.197  1.00  0.00      A2
ATOM  912 CA  TRP  119      57.575  69.142  -8.399  1.00 58.98      A2
ATOM  913 CB  TRP  119      57.392  70.367  -7.477  1.00 59.84      A2
ATOM  914 CG  TRP  119      58.051  71.529  -8.196  1.00 62.64      A2
ATOM  915 CD2 TRP  119      57.596  72.211  -9.307  1.00 61.78      A2
ATOM  916 CE2 TRP  119      58.699  72.955  -9.643  1.00 62.55      A2
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FIGURE 5

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ATOM  917 CE3 TRP  119      56.465  72.514 -10.080  1.00 66.02      A2
ATOM  918 CD1 TRP  119      59.322  71.870  -7.863  1.00 64.12      A2
ATOM  919 NE1 TRP  119      59.680  72.727  -8.784  1.00 65.00      A2
ATOM  920 HE1 TRP  119      60.568  73.140  -8.828  1.00  0.00      A2
ATOM  921 CZ2 TRP  119      58.726  73.794 -10.714  1.00 62.90      A2
ATOM  922 CZ3 TRP  119      56.469  73.157 -11.170  1.00 65.18      A2
ATOM  923 CH2 TRP  119      57.591  73.887 -11.481  1.00 64.40      A2
ATOM  924 C   TRP  119      59.021  68.664  -8.352  1.00 61.26      A2
ATOM  925 O   TRP  119      59.748  68.788  -9.343  1.00 62.12      A2
ATOM  926 N   GLN  120      59.447  68.065  -7.249  1.00 62.91      A2
ATOM  927 H   GLN  120      58.811  67.961  -6.519  1.00  0.00      A2
ATOM  928 CA  GLN  120      60.786  67.504  -7.113  1.00 65.16      A2
ATOM  929 CB  GLN  120      60.900  66.800  -5.780  1.00 66.56      A2
ATOM  930 CG  GLN  120      60.627  67.678  -4.582  1.00 67.18      A2
ATOM  931 CD  GLN  120      60.725  66.907  -3.284  1.00 67.77      A2
ATOM  932 OE1 GLN  120      61.221  67.465  -2.319  1.00 69.31      A2
ATOM  933 NE2 GLN  120      60.305  65.654  -3.129  1.00 67.39      A2
ATOM  934 HE21 GLN  120     59.903  65.174  -3.877  1.00  0.00      A2
ATOM  935 HE22 GLN  120     60.441  65.282  -2.234  1.00  0.00      A2
ATOM  936 C   GLN  120      61.169  66.509  -8.222  1.00 66.22      A2
ATOM  937 O   GLN  120      62.326  66.421  -8.662  1.00 66.50      A2
ATOM  938 N   GLN  121      60.202  65.745  -8.706  1.00 67.10      A2
ATOM  939 H   GLN  121      59.307  65.754  -8.303  1.00  0.00      A2
ATOM  940 CA  GLN  121      60.480  64.878  -9.812  1.00 68.66      A2
ATOM  941 CB  GLN  121      59.292  63.971 -10.070  1.00 67.96      A2
ATOM  942 CG  GLN  121      59.614  62.937 -11.128  1.00 68.89      A2
ATOM  943 CD  GLN  121      60.940  62.236 -10.852  1.00 71.37      A2
ATOM  944 OE1 GLN  121      61.212  61.706  -9.777  1.00 71.70      A2
ATOM  945 NE2 GLN  121      61.879  62.262 -11.786  1.00 74.41      A2
ATOM  946 HE21 GLN  121     61.707  62.729 -12.627  1.00  0.00      A2
ATOM  947 HE22 GLN  121     62.736  61.859 -11.541  1.00  0.00      A2
ATOM  948 C   GLN  121      60.760  65.743 -11.045  1.00 70.48      A2
ATOM  949 O   GLN  121      61.671  65.436 -11.827  1.00 70.94      A2
ATOM  950 N   MET  122      60.019  66.846 -11.236  1.00 71.67      A2
ATOM  951 H   MET  122      59.351  67.087 -10.555  1.00  0.00      A2
ATOM  952 CA  MET  122      60.190  67.688 -12.412  1.00 72.62      A2
ATOM  953 CB  MET  122      59.173  68.819 -12.448  1.00 73.12      A2
ATOM  954 CG  MET  122      57.880  68.343 -13.083  1.00 73.64      A2
ATOM  955 SD  MET  122      56.669  69.662 -13.295  1.00 75.44      A2
ATOM  956 CE  MET  122      55.695  69.349 -11.861  1.00 76.43      A2
ATOM  957 C   MET  122      61.566  68.281 -12.411  1.00 73.22      A2
ATOM  958 O   MET  122      62.240  68.287 -13.441  1.00 73.03      A2
ATOM  959 N   GLU  123      61.991  68.697 -11.223  1.00 74.74      A2
ATOM  960 H   GLU  123      61.372  68.617 -10.466  1.00  0.00      A2
ATOM  961 CA  GLU  123      63.305  69.262 -11.018  1.00 75.95      A2
ATOM  962 CB  GLU  123      63.484  69.665  -9.597  1.00 75.72      A2
ATOM  963 CG  GLU  123      62.644  70.906  -9.500  1.00 79.11      A2
ATOM  964 CD  GLU  123      62.651  71.529  -8.122  1.00 83.02      A2
ATOM  965 OE1 GLU  123      62.741  72.763  -8.057  1.00 84.15      A2
ATOM  966 OE2 GLU  123      62.543  70.789  -7.133  1.00 84.45      A2
ATOM  967 C   GLU  123      64.381  68.280 -11.586  1.00 77.17      A2
ATOM  968 O   GLU  123      65.092  68.558 -12.356  1.00 78.22      A2
ATOM  969 N   GLU  124      64.504  67.110 -10.765  1.00 77.66      A2
ATOM  970 H   GLU  124      63.867  66.852 -10.060  1.00  0.00      A2
ATOM  971 CA  GLU  124      65.574  66.215 -11.167  1.00 78.47      A2
ATOM  972 CB  GLU  124      65.600  65.051 -10.195  1.00 80.79      A2
ATOM  973 CG  GLU  124      64.387  64.132 -10.150  1.00 84.29      A2
ATOM  974 CD  GLU  124      64.375  63.248  -8.908  1.00 85.51      A2
ATOM  975 OE1 GLU  124      64.733  63.729  -7.824  1.00 86.84      A2
ATOM  976 OE2 GLU  124      64.006  62.075  -9.024  1.00 86.39      A2
ATOM  977 C   GLU  124      65.534  65.705 -12.612  1.00 78.01      A2
ATOM  978 O   GLU  124      66.480  65.057 -13.060  1.00 78.91      A2
ATOM  979 N   LEU  125      64.460  65.943 -13.363  1.00 77.11      A2
ATOM  980 H   LEU  125      63.666  66.340 -12.945  1.00  0.00      A2
ATOM  981 CA  LEU  125      64.387  65.583 -14.771  1.00 76.23      A2
ATOM  982 CB  LEU  125      63.061  64.832 -14.952  1.00 76.88      A2
ATOM  983 CG  LEU  125      62.392  64.382 -16.263  1.00 76.63      A2
ATOM  984 CD1 LEU  125      63.350  63.754 -17.276  1.00 76.67      A2
ATOM  985 CD2 LEU  125      61.309  63.402 -15.839  1.00 75.89      A2
ATOM  986 C   LEU  125      64.506  66.827 -15.648  1.00 75.84      A2
ATOM  987 O   LEU  125      64.360  66.788 -16.871  1.00 75.36      A2
ATOM  988 N   GLY  126      64.759  67.968 -15.027  1.00 75.90      A2
ATOM  989 H   GLY  126      64.741  67.976 -14.056  1.00  0.00      A2
ATOM  990 CA  GLY  126      64.968  69.213 -15.736  1.00 77.58      A2
ATOM  991 C   GLY  126      63.697  69.814 -16.330  1.00 78.63      A2
ATOM  992 O   GLY  126      63.735  70.736 -17.146  1.00 78.55      A2
ATOM  993 N   MET  127      62.524  69.343 -15.933  1.00 80.08      A2
ATOM  994 H   MET  127      62.522  68.603 -15.293  1.00  0.00      A2
ATOM  995 CA  MET  127      61.266  69.902 -16.415  1.00 81.46      A2
ATOM  996 CB  MET  127      60.191  68.802 -16.361  1.00 81.86      A2
ATOM  997 CG  MET  127      60.708  67.599 -17.147  1.00 82.66      A2
ATOM  998 SD  MET  127      59.682  66.115 -17.282  1.00 83.70      A2
ATOM  999 CE  MET  127      60.236  65.620 -18.900  1.00 84.23      A2
ATOM 1000 C   MET  127      60.847  71.131 -15.599  1.00 82.18      A2
ATOM 1001 OT1 MET  127      60.116  71.958 -16.142  1.00 83.86      A2
ATOM 1002 OT2 MET  127      61.267  71.285 -14.446  1.00 82.04      A2
ATOM 1003 CB  MET  138      39.323  80.595  -4.492  1.00 59.39      A3
ATOM 1004 CG  MET  138      40.123  79.298  -4.421  1.00 57.97      A3
ATOM 1005 SD  MET  138      40.561  78.973  -6.145  1.00 60.85      A3
ATOM 1006 CE  MET  138      41.129  77.310  -6.351  1.00 61.48      A3
ATOM 1007 C   MET  138      37.021  81.072  -5.454  1.00 60.26      A3
ATOM 1008 O   MET  138      36.832  82.262  -5.181  1.00 62.98      A3
ATOM 1009 HT1 MET  138      38.497  82.600  -6.075  1.00  0.00      A3
ATOM 1010 HT2 MET  138      38.313  81.757  -7.529  1.00  0.00      A3
ATOM 1011 N   MET  138      38.839  81.784  -6.639  1.00 60.49      A3
ATOM 1012 HT3 MET  138      39.865  81.816  -6.768  1.00  0.00      A3
ATOM 1013 CA  MET  138      38.445  80.672  -5.787  1.00 60.51      A3
ATOM 1014 N   PRO  139      35.995  80.242  -5.612  1.00 57.82      A3
ATOM 1015 CD  PRO  139      36.028  79.060  -6.448  1.00 58.10      A3
ATOM 1016 CA  PRO  139      34.654  80.538  -5.142  1.00 54.67      A3
ATOM 1017 CB  PRO  139      33.870  79.323  -5.525  1.00 54.54      A3
ATOM 1018 CG  PRO  139      34.945  78.290  -5.755  1.00 58.26      A3
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FIGURE 5

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ATOM  1019  C   PRO  139      34.588  80.675  -3.664  1.00 52.24      A3
ATOM  1020  O   PRO  139      35.507  80.623  -2.882  1.00 51.89      A3
ATOM  1021  N   ALA  140      33.499  81.547  -3.342  1.00 49.86      A3
ATOM  1022  H   ALA  140      32.789  81.676  -4.005  1.00  0.00      A3
ATOM  1023  CA  ALA  140      33.234  81.926  -1.994  1.00 49.39      A3
ATOM  1024  CB  ALA  140      32.966  83.413  -1.895  1.00 49.94      A3
ATOM  1025  C   ALA  140      31.978  81.153  -1.590  1.00 49.25      A3
ATOM  1026  O   ALA  140      30.889  81.162  -2.205  1.00 49.06      A3
ATOM  1027  N   PHE  141      32.293  80.442  -0.506  1.00 47.48      A3
ATOM  1028  H   PHE  141      33.190  80.550  -0.122  1.00  0.00      A3
ATOM  1029  CA  PHE  141      31.401  79.552   0.208  1.00 45.66      A3
ATOM  1030  CB  PHE  141      32.215  78.305   0.792  1.00 40.28      A3
ATOM  1031  CG  PHE  141      32.684  77.404  -0.349  1.00 35.35      A3
ATOM  1032  CD1 PHE  141      31.800  76.591  -1.006  1.00 34.39      A3
ATOM  1033  CD2 PHE  141      33.966  77.497  -0.830  1.00 37.69      A3
ATOM  1034  CE1 PHE  141      32.174  75.895  -2.133  1.00 34.00      A3
ATOM  1035  CE2 PHE  141      34.358  76.807  -1.956  1.00 36.69      A3
ATOM  1036  CZ  PHE  141      33.449  76.001  -2.614  1.00 37.29      A3
ATOM  1037  C   PHE  141      31.003  80.580   1.242  1.00 46.54      A3
ATOM  1038  O   PHE  141      31.584  80.664   2.317  1.00 48.26      A3
ATOM  1039  N   ALA  142      30.067  81.452   0.843  1.00 47.38      A3
ATOM  1040  H   ALA  142      29.624  81.295  -0.020  1.00  0.00      A3
ATOM  1041  CA  ALA  142      29.581  82.564   1.668  1.00 46.06      A3
ATOM  1042  CB  ALA  142      28.731  83.546   0.879  1.00 45.04      A3
ATOM  1043  C   ALA  142      28.703  82.132   2.802  1.00 45.27      A3
ATOM  1044  O   ALA  142      28.343  83.002   3.584  1.00 47.38      A3
ATOM  1045  N   SER  143      28.318  80.860   2.899  1.00 43.36      A3
ATOM  1046  H   SER  143      28.724  80.201   2.303  1.00  0.00      A3
ATOM  1047  CA  SER  143      27.377  80.392   3.897  1.00 41.94      A3
ATOM  1048  CB  SER  143      26.036  80.129   3.181  1.00 44.17      A3
ATOM  1049  OG  SER  143      25.323  78.918   3.536  1.00 48.18      A3
ATOM  1050  HG  SER  143      24.455  78.974   3.098  1.00  0.00      A3
ATOM  1051  C   SER  143      27.877  79.145   4.602  1.00 39.79      A3
ATOM  1052  O   SER  143      28.763  78.452   4.132  1.00 38.50      A3
ATOM  1053  N   ALA  144      27.218  78.775   5.683  1.00 39.10      A3
ATOM  1054  H   ALA  144      26.449  79.312   5.960  1.00  0.00      A3
ATOM  1055  CA  ALA  144      27.566  77.586   6.411  1.00 39.22      A3
ATOM  1056  CB  ALA  144      26.982  77.598   7.802  1.00 36.97      A3
ATOM  1057  C   ALA  144      26.964  76.420   5.627  1.00 41.58      A3
ATOM  1058  O   ALA  144      27.706  75.448   5.444  1.00 42.07      A3
ATOM  1059  N   PHE  145      25.719  76.407   5.076  1.00 40.77      A3
ATOM  1060  H   PHE  145      25.149  77.203   5.110  1.00  0.00      A3
ATOM  1061  CA  PHE  145      25.307  75.234   4.312  1.00 39.31      A3
ATOM  1062  CB  PHE  145      23.877  75.396   3.798  1.00 36.46      A3
ATOM  1063  CG  PHE  145      23.477  74.452   2.641  1.00 31.91      A3
ATOM  1064  CD1 PHE  145      23.579  74.900   1.323  1.00 29.02      A3
ATOM  1065  CD2 PHE  145      23.013  73.185   2.916  1.00 29.40      A3
ATOM  1066  CE1 PHE  145      23.225  74.100   0.277  1.00 28.34      A3
ATOM  1067  CE2 PHE  145      22.661  72.389   1.858  1.00 28.80      A3
ATOM  1068  CZ  PHE  145      22.764  72.831   0.549  1.00 30.58      A3
ATOM  1069  C   PHE  145      26.266  75.071   3.120  1.00 40.44      A3
ATOM  1070  O   PHE  145      26.556  73.938   2.697  1.00 40.55      A3
ATOM  1071  N   GLN  146      26.745  76.232   2.619  1.00 39.11      A3
ATOM  1072  H   GLN  146      26.437  77.073   3.015  1.00  0.00      A3
ATOM  1073  CA  GLN  146      27.660  76.263   1.511  1.00 48.01      A3
ATOM  1074  CB  GLN  146      27.907  77.644   1.054  1.00 48.92      A3
ATOM  1075  CG  GLN  146      26.884  78.066   0.049  1.00 46.26      A3
ATOM  1076  CD  GLN  146      27.171  79.440  -0.522  1.00 45.37      A3
ATOM  1077  OE1 GLN  146      27.851  80.253   0.033  1.00 47.57      A3
ATOM  1078  NE2 GLN  146      26.689  79.793  -1.692  1.00 47.50      A3
ATOM  1079 HE21 GLN  146      26.149  79.149  -2.190  1.00  0.00      A3
ATOM  1080 HE22 GLN  146      26.913  80.690  -2.021  1.00  0.00      A3
ATOM  1081  C   GLN  146      29.005  75.670   1.836  1.00 37.25      A3
ATOM  1082  O   GLN  146      29.634  75.093   0.950  1.00 38.28      A3
ATOM  1083  N   ARG  147      29.511  75.775   3.054  1.00 36.37      A3
ATOM  1084  H   ARG  147      29.044  76.300   3.738  1.00  0.00      A3
ATOM  1085  CA  ARG  147      30.798  75.180   3.357  1.00 35.68      A3
ATOM  1086  CB  ARG  147      31.299  75.574   4.713  1.00 37.12      A3
ATOM  1087  CG  ARG  147      31.730  77.016   4.697  1.00 42.68      A3
ATOM  1088  CD  ARG  147      32.034  77.494   6.093  1.00 49.54      A3
ATOM  1089  NE  ARG  147      32.674  78.774   5.877  1.00 58.21      A3
ATOM  1090  HE  ARG  147      32.475  79.252   5.045  1.00  0.00      A3
ATOM  1091  CZ  ARG  147      33.519  79.373   6.742  1.00 62.77      A3
ATOM  1092  NH1 ARG  147      33.905  78.868   7.936  1.00 64.96      A3
ATOM  1093 HH11 ARG  147      34.545  79.379   8.510  1.00  0.00      A3
ATOM  1094 HH12 ARG  147      33.561  77.980   8.239  1.00  0.00      A3
ATOM  1095  NH2 ARG  147      33.960  80.584   6.403  1.00 64.80      A3
ATOM  1096 HH21 ARG  147      34.599  81.069   6.999  1.00  0.00      A3
ATOM  1097 HH22 ARG  147      33.665  80.996   5.541  1.00  0.00      A3
ATOM  1098  C   ARG  147      30.570  73.702   3.387  1.00 34.91      A3
ATOM  1099  O   ARG  147      31.233  73.050   2.539  1.00 34.56      A3
ATOM  1100  N   ALA  148      29.544  73.194   4.040  1.00 33.44      A3
ATOM  1101  H   ALA  148      28.926  73.818   4.482  1.00  0.00      A3
ATOM  1102  CA  ALA  148      29.358  71.754   4.172  1.00 33.92      A3
ATOM  1103  CB  ALA  148      28.217  71.426   5.163  1.00 32.85      A3
ATOM  1104  C   ALA  148      29.077  71.095   2.845  1.00 33.40      A3
ATOM  1105  O   ALA  148      29.765  70.141   2.457  1.00 34.31      A3
ATOM  1106  N   ALA  149      28.169  71.657   2.077  1.00 32.60      A3
ATOM  1107  H   ALA  149      27.662  72.424   2.411  1.00  0.00      A3
ATOM  1108  CA  ALA  149      27.890  71.134   0.757  1.00 32.70      A3
ATOM  1109  CB  ALA  149      26.595  71.774   0.299  1.00 31.91      A3
ATOM  1110  C   ALA  149      29.032  71.381  -0.258  1.00 33.75      A3
ATOM  1111  O   ALA  149      29.208  70.661  -1.264  1.00 34.49      A3
ATOM  1112  N   GLY  150      29.867  72.401  -0.052  1.00 33.58      A3
ATOM  1113  H   GLY  150      29.724  73.035   0.682  1.00  0.00      A3
ATOM  1114  CA  GLY  150      31.017  72.608  -0.913  1.00 31.79      A3
ATOM  1115  C   GLY  150      32.113  71.620  -0.478  1.00 31.49      A3
ATOM  1116  O   GLY  150      32.997  71.261  -1.265  1.00 31.77      A3
ATOM  1117  N   GLY  151      32.075  71.161   0.773  1.00 29.84      A3
ATOM  1118  H   GLY  151      31.412  71.524   1.394  1.00  0.00      A3
ATOM  1119  CA  GLY  151      33.018  70.166   1.243  1.00 32.16      A3
ATOM  1120  C   GLY  151      32.764  68.909   0.409  1.00 33.98      A3
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FIGURE 5

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ATOM  1121  O   GLY   151      33.664  68.501  -0.349  1.00 35.66      A3
ATOM  1122  N   VAL   152      31.486  68.418   0.451  1.00 31.87      A3
ATOM  1123  H   VAL   152      30.867  68.906   1.040  1.00  0.00      A3
ATOM  1124  CA  VAL   152      30.978  67.240  -0.275  1.00 29.61      A3
ATOM  1125  CB  VAL   152      29.419  67.145  -0.125  1.00 27.63      A3
ATOM  1126  CG1 VAL   152      28.883  66.035  -0.976  1.00 27.37      A3
ATOM  1127  CG2 VAL   152      29.002  66.786   1.279  1.00 24.74      A3
ATOM  1128  C   VAL   152      31.351  67.294  -1.762  1.00 29.91      A3
ATOM  1129  O   VAL   152      31.805  66.329  -2.393  1.00 31.75      A3
ATOM  1130  N   LEU   153      31.236  68.452  -2.361  1.00 29.26      A3
ATOM  1131  H   LEU   153      30.881  69.219  -1.860  1.00  0.00      A3
ATOM  1132  CA  LEU   153      31.559  68.607  -3.756  1.00 26.77      A3
ATOM  1133  CB  LEU   153      30.881  69.858  -4.160  1.00 28.22      A3
ATOM  1134  CG  LEU   153      29.943  69.894  -5.316  1.00 30.67      A3
ATOM  1135  CD1 LEU   153      28.580  69.281  -5.090  1.00 26.48      A3
ATOM  1136  CD2 LEU   153      29.741  71.365  -5.496  1.00 34.46      A3
ATOM  1137  C   LEU   153      33.032  68.628  -4.111  1.00 26.08      A3
ATOM  1138  O   LEU   153      33.419  68.187  -5.212  1.00 26.78      A3
ATOM  1139  N   VAL   154      33.902  69.180  -3.269  1.00 26.12      A3
ATOM  1140  H   VAL   154      33.589  69.557  -2.416  1.00  0.00      A3
ATOM  1141  CA  VAL   154      35.330  69.259  -3.611  1.00 26.23      A3
ATOM  1142  CB  VAL   154      36.057  70.299  -2.692  1.00 26.51      A3
ATOM  1143  CG1 VAL   154      37.578  70.188  -2.942  1.00 25.01      A3
ATOM  1144  CG2 VAL   154      35.528  71.728  -2.945  1.00 27.82      A3
ATOM  1145  C   VAL   154      35.933  67.850  -3.375  1.00 26.80      A3
ATOM  1146  O   VAL   154      36.678  67.363  -4.229  1.00 26.27      A3
ATOM  1147  N   ALA   155      35.635  67.241  -2.199  1.00 24.76      A3
ATOM  1148  H   ALA   155      35.084  67.758  -1.570  1.00  0.00      A3
ATOM  1149  CA  ALA   155      36.095  65.940  -1.782  1.00 25.21      A3
ATOM  1150  CB  ALA   155      35.463  65.572  -0.457  1.00 25.25      A3
ATOM  1151  C   ALA   155      35.708  64.946  -2.841  1.00 26.94      A3
ATOM  1152  O   ALA   155      36.594  64.288  -3.398  1.00 26.76      A3
ATOM  1153  N   SER   156      34.450  64.982  -3.282  1.00 29.96      A3
ATOM  1154  H   SER   156      33.790  65.577  -2.868  1.00  0.00      A3
ATOM  1155  CA  SER   156      34.034  64.105  -4.354  1.00 32.17      A3
ATOM  1156  CB  SER   156      32.531  64.319  -4.544  1.00 34.23      A3
ATOM  1157  OG  SER   156      32.000  64.195  -5.879  1.00 39.35      A3
ATOM  1158  HG  SER   156      31.120  63.815  -5.851  1.00  0.00      A3
ATOM  1159  C   SER   156      34.845  64.338  -5.632  1.00 33.46      A3
ATOM  1160  O   SER   156      35.411  63.380  -6.174  1.00 34.62      A3
ATOM  1161  N   HIS   157      35.054  65.576  -6.133  1.00 33.90      A3
ATOM  1162  H   HIS   157      34.771  66.349  -5.605  1.00  0.00      A3
ATOM  1163  CA  HIS   157      35.821  65.773  -7.383  1.00 31.19      A3
ATOM  1164  CB  HIS   157      35.707  67.209  -7.900  1.00 32.59      A3
ATOM  1165  CG  HIS   157      34.369  67.449  -8.566  1.00 31.11      A3
ATOM  1166  CD2 HIS   157      34.127  67.394  -9.928  1.00 30.78      A3
ATOM  1167  ND1 HIS   157      33.223  67.666  -7.942  1.00 32.36      A3
ATOM  1168  HD1 HIS   157      33.080  67.773  -6.979  1.00  0.00      A3
ATOM  1169  CE1 HIS   157      32.293  67.732  -8.875  1.00 32.01      A3
ATOM  1170  NE2 HIS   157      32.838  67.571 -10.060  1.00 29.18      A3
ATOM  1171  HE2 HIS   157      32.327  67.621 -10.895  1.00  0.00      A3
ATOM  1172  C   HIS   157      37.291  65.476  -7.269  1.00 29.68      A3
ATOM  1173  O   HIS   157      37.950  65.059  -8.219  1.00 29.65      A3
ATOM  1174  N   LEU   158      37.801  65.669  -6.071  1.00 29.24      A3
ATOM  1175  H   LEU   158      37.213  65.901  -5.326  1.00  0.00      A3
ATOM  1176  CA  LEU   158      39.216  65.479  -5.826  1.00 31.94      A3
ATOM  1177  CB  LEU   158      39.609  65.949  -4.373  1.00 28.66      A3
ATOM  1178  CG  LEU   158      41.008  65.751  -3.859  1.00 24.42      A3
ATOM  1179  CD1 LEU   158      41.990  66.378  -4.776  1.00 20.87      A3
ATOM  1180  CD2 LEU   158      41.099  66.330  -2.477  1.00 24.86      A3
ATOM  1181  C   LEU   158      39.468  63.994  -6.027  1.00 31.46      A3
ATOM  1182  O   LEU   158      40.298  63.609  -6.844  1.00 30.58      A3
ATOM  1183  N   GLN   159      38.652  63.225  -5.340  1.00 33.54      A3
ATOM  1184  H   GLN   159      38.011  63.676  -4.748  1.00  0.00      A3
ATOM  1185  CA  GLN   159      38.594  61.792  -5.442  1.00 35.73      A3
ATOM  1186  CB  GLN   159      37.308  61.492  -4.813  1.00 37.26      A3
ATOM  1187  CG  GLN   159      37.064  60.063  -4.520  1.00 45.01      A3
ATOM  1188  CD  GLN   159      37.755  59.611  -3.256  1.00 46.24      A3
ATOM  1189  OE1 GLN   159      38.142  58.443  -3.232  1.00 48.29      A3
ATOM  1190  NE2 GLN   159      37.936  60.456  -2.224  1.00 47.82      A3
ATOM  1191 HE21 GLN   159      37.575  61.364  -2.289  1.00  0.00      A3
ATOM  1192 HE22 GLN   159      38.412  60.101  -1.447  1.00  0.00      A3
ATOM  1193  C   GLN   159      38.686  61.381  -6.921  1.00 36.24      A3
ATOM  1194  O   GLN   159      39.632  60.690  -7.324  1.00 38.97      A3
ATOM  1195  N   SER   160      37.824  61.896  -7.796  1.00 35.48      A3
ATOM  1196  H   SER   160      37.142  62.540  -7.498  1.00  0.00      A3
ATOM  1197  CA  SER   160      37.869  61.564  -9.203  1.00 34.96      A3
ATOM  1198  CB  SER   160      36.645  62.100  -9.863  1.00 37.54      A3
ATOM  1199  OG  SER   160      35.587  62.434  -8.942  1.00 44.81      A3
ATOM  1200  HG  SER   160      35.340  61.689  -8.387  1.00  0.00      A3
ATOM  1201  C   SER   160      39.090  62.095  -9.922  1.00 31.65      A3
ATOM  1202  O   SER   160      39.605  61.382 -10.785  1.00 35.42      A3
ATOM  1203  N   PHE   161      39.615  63.293  -9.595  1.00 33.82      A3
ATOM  1204  H   PHE   161      39.203  63.796  -8.864  1.00  0.00      A3
ATOM  1205  CA  PHE   161      40.820  63.850 -10.218  1.00 31.21      A3
ATOM  1206  CB  PHE   161      41.110  65.254  -9.629  1.00 28.28      A3
ATOM  1207  CG  PHE   161      42.455  65.881 -10.062  1.00 24.92      A3
ATOM  1208  CD1 PHE   161      42.696  66.228 -11.389  1.00 22.98      A3
ATOM  1209  CD2 PHE   161      43.464  66.021  -9.135  1.00 23.63      A3
ATOM  1210  CE1 PHE   161      43.941  66.695 -11.767  1.00 21.06      A3
ATOM  1211  CE2 PHE   161      44.701  66.495  -9.528  1.00 20.28      A3
ATOM  1212  CZ  PHE   161      44.939  66.826 -10.832  1.00 17.04      A3
ATOM  1213  C   PHE   161      42.008  62.907  -9.943  1.00 31.77      A3
ATOM  1214  O   PHE   161      42.786  62.578 -10.845  1.00 32.64      A3
ATOM  1215  N   LEU   162      42.117  62.434  -8.690  1.00 31.67      A3
ATOM  1216  H   LEU   162      41.420  62.691  -8.054  1.00  0.00      A3
ATOM  1217  CA  LEU   162      43.186  61.574  -8.232  1.00 31.29      A3
ATOM  1218  CB  LEU   162      43.204  61.433  -6.743  1.00 25.84      A3
ATOM  1219  CG  LEU   162      43.693  62.674  -6.003  1.00 26.02      A3
ATOM  1220  CD1 LEU   162      43.594  62.455  -4.516  1.00 25.24      A3
ATOM  1221  CD2 LEU   162      45.107  62.994  -6.415  1.00 27.04      A3
ATOM  1222  C   LEU   162      43.061  60.212  -8.813  1.00 34.24      A3
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FIGURE 5

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ATOM  1223  O  LEU  162      44.107  59.654  -9.070  1.00 36.51      A3
ATOM  1224  N  GLU  163      41.926  59.589  -9.082  1.00 37.24      A3
ATOM  1225  H  GLU  163      41.072  60.002  -8.826  1.00  0.00      A3
ATOM  1226  CA GLU  163      41.975  58.327  -9.771  1.00 40.47      A3
ATOM  1227  CB GLU  163      40.566  57.716  -9.835  1.00 45.38      A3
ATOM  1228  CG GLU  163      40.264  56.975  -8.526  1.00 51.84      A3
ATOM  1229  CD GLU  163      41.291  55.889  -8.126  1.00 57.97      A3
ATOM  1230  OE1 GLU  163      40.897  54.722  -8.092  1.00 62.01      A3
ATOM  1231  OE2 GLU  163      42.466  56.180  -7.832  1.00 59.17      A3
ATOM  1232  C  GLU  163      42.586  58.430 -11.142  1.00 41.34      A3
ATOM  1233  O  GLU  163      43.456  57.633 -11.486  1.00 42.17      A3
ATOM  1234  N  VAL  164      42.257  59.436 -11.920  1.00 42.28      A3
ATOM  1235  H  VAL  164      41.589  60.091 -11.615  1.00  0.00      A3
ATOM  1236  CA VAL  164      42.911  59.609 -13.187  1.00 44.13      A3
ATOM  1237  CB VAL  164      42.207  60.711 -13.940  1.00 45.52      A3
ATOM  1238  CG1 VAL  164      42.892  60.975 -15.278  1.00 48.79      A3
ATOM  1239  CG2 VAL  164      40.786  60.269 -14.226  1.00 46.09      A3
ATOM  1240  C  VAL  164      44.386  59.933 -12.991  1.00 46.13      A3
ATOM  1241  O  VAL  164      45.192  59.473 -13.794  1.00 45.99      A3
ATOM  1242  N  SER  165      44.879  60.677 -12.006  1.00 49.51      A3
ATOM  1243  H  SER  165      44.287  61.173 -11.396  1.00  0.00      A3
ATOM  1244  CA SER  165      46.325  60.845 -11.895  1.00 53.44      A3
ATOM  1245  CB SER  165      46.715  61.796 -10.775  1.00 54.77      A3
ATOM  1246  OG SER  165      46.049  61.618  -9.530  1.00 59.99      A3
ATOM  1247  HG SER  165      45.997  60.694  -9.261  1.00  0.00      A3
ATOM  1248  C  SER  165      46.958  59.502 -11.630  1.00 55.15      A3
ATOM  1249  O  SER  165      48.028  59.227 -12.148  1.00 55.02      A3
ATOM  1250  N  TYR  166      46.239  58.645 -10.900  1.00 58.57      A3
ATOM  1251  H  TYR  166      45.374  58.948 -10.549  1.00  0.00      A3
ATOM  1252  CA TYR  166      46.617  57.273 -10.625  1.00 61.42      A3
ATOM  1253  CB TYR  166      45.543  56.653  -9.680  1.00 64.05      A3
ATOM  1254  CG TYR  166      45.502  55.138  -9.682  1.00 69.00      A3
ATOM  1255  CD1 TYR  166      44.389  54.501 -10.185  1.00 71.64      A3
ATOM  1256  CE1 TYR  166      44.367  53.130 -10.283  1.00 73.15      A3
ATOM  1257  CD2 TYR  166      46.594  54.409  -9.257  1.00 71.27      A3
ATOM  1258  CE2 TYR  166      46.584  53.040  -9.346  1.00 72.92      A3
ATOM  1259  CZ  TYR  166      45.468  52.417  -9.862  1.00 75.71      A3
ATOM  1260  OH  TYR  166      45.474  51.038 -10.016  1.00 80.61      A3
ATOM  1261  HH  TYR  166      44.571  50.736 -10.134  1.00  0.00      A3
ATOM  1262  C  TYR  166      46.712  56.567 -11.987  1.00 62.34      A3
ATOM  1263  O  TYR  166      47.766  55.981 -12.282  1.00 63.25      A3
ATOM  1264  N  ALA  167      45.727  56.622 -12.884  1.00 61.27      A3
ATOM  1265  H  ALA  167      44.893  57.089 -12.678  1.00  0.00      A3
ATOM  1266  CA ALA  167      45.933  55.982 -14.159  1.00 61.47      A3
ATOM  1267  CB ALA  167      44.608  55.904 -14.904  1.00 60.98      A3
ATOM  1268  C  ALA  167      46.982  56.694 -15.020  1.00 62.19      A3
ATOM  1269  O  ALA  167      47.719  56.000 -15.734  1.00 62.63      A3
ATOM  1270  N  VAL  168      47.210  58.011 -14.991  1.00 63.37      A3
ATOM  1271  H  VAL  168      46.756  58.570 -14.330  1.00  0.00      A3
ATOM  1272  CA VAL  168      48.174  58.593 -15.923  1.00 65.62      A3
ATOM  1273  CB VAL  168      48.061  60.121 -16.131  1.00 66.30      A3
ATOM  1274  CG1 VAL  168      46.687  60.431 -16.706  1.00 66.78      A3
ATOM  1275  CG2 VAL  168      48.278  60.879 -14.840  1.00 68.47      A3
ATOM  1276  C  VAL  168      49.579  58.339 -15.469  1.00 66.45      A3
ATOM  1277  O  VAL  168      50.458  58.183 -16.302  1.00 66.22      A3
ATOM  1278  N  LEU  169      49.823  58.241 -14.177  1.00 68.83      A3
ATOM  1279  H  LEU  169      49.102  58.404 -13.536  1.00  0.00      A3
ATOM  1280  CA LEU  169      51.141  57.899 -13.695  1.00 71.81      A3
ATOM  1281  CB LEU  169      51.249  58.228 -12.188  1.00 71.53      A3
ATOM  1282  CG LEU  169      51.137  59.732 -11.813  1.00 70.68      A3
ATOM  1283  CD1 LEU  169      51.187  59.826 -10.298  1.00 69.39      A3
ATOM  1284  CD2 LEU  169      52.223  60.580 -12.491  1.00 68.49      A3
ATOM  1285  C  LEU  169      51.333  56.414 -13.979  1.00 73.61      A3
ATOM  1286  O  LEU  169      52.408  56.013 -14.429  1.00 74.75      A3
ATOM  1287  N  ARG  170      50.309  55.583 -13.819  1.00 75.45      A3
ATOM  1288  H  ARG  170      49.488  55.923 -13.399  1.00  0.00      A3
ATOM  1289  CA ARG  170      50.364  54.179 -14.199  1.00 78.17      A3
ATOM  1290  CB ARG  170      48.944  53.642 -14.004  1.00 78.45      A3
ATOM  1291  CG ARG  170      48.394  52.506 -14.871  1.00 78.17      A3
ATOM  1292  CD ARG  170      48.744  51.181 -14.271  1.00 77.25      A3
ATOM  1293  NE ARG  170      48.123  51.120 -12.970  1.00 76.15      A3
ATOM  1294  HE ARG  170      47.245  51.528 -12.824  1.00  0.00      A3
ATOM  1295  CZ ARG  170      48.758  50.547 -11.970  1.00 76.14      A3
ATOM  1296  NH1 ARG  170      49.973  50.017 -12.112  1.00 76.84      A3
ATOM  1297 HH11 ARG  170      50.441  50.030 -12.994  1.00  0.00      A3
ATOM  1298 HH12 ARG  170      50.406  49.570 -11.329  1.00  0.00      A3
ATOM  1299  NH2 ARG  170      48.147  50.492 -10.806  1.00 77.02      A3
ATOM  1300 HH21 ARG  170      47.237  50.890 -10.714  1.00  0.00      A3
ATOM  1301 HH22 ARG  170      48.586  50.052 -10.023  1.00  0.00      A3
ATOM  1302  C  ARG  170      50.870  54.052 -15.647  1.00 79.84      A3
ATOM  1303  O  ARG  170      51.924  53.470 -15.908  1.00 80.07      A3
ATOM  1304  N  HIS  171      50.193  54.663 -16.611  1.00 81.38      A3
ATOM  1305  H  HIS  171      49.433  55.234 -16.359  1.00  0.00      A3
ATOM  1306  CA HIS  171      50.663  54.597 -17.970  1.00 84.03      A3
ATOM  1307  CB HIS  171      49.590  55.054 -18.902  1.00 86.82      A3
ATOM  1308  CG HIS  171      48.496  54.037 -19.147  1.00 90.73      A3
ATOM  1309  CD2 HIS  171      47.467  53.765 -18.272  1.00 91.35      A3
ATOM  1310  ND1 HIS  171      48.308  53.301 -20.248  1.00 92.24      A3
ATOM  1311  HD1 HIS  171      48.887  53.287 -21.044  1.00  0.00      A3
ATOM  1312  CE1 HIS  171      47.204  52.605 -20.077  1.00 92.41      A3
ATOM  1313  NE2 HIS  171      46.711  52.892 -18.891  1.00 92.59      A3
ATOM  1314  HE2 HIS  171      45.884  52.511 -18.518  1.00  0.00      A3
ATOM  1315  C  HIS  171      51.907  55.446 -18.232  1.00 85.42      A3
ATOM  1316  O  HIS  171      52.440  55.352 -19.344  1.00 85.98      A3
ATOM  1317  N  LEU  172      52.359  56.307 -17.302  1.00 86.13      A3
ATOM  1318  H  LEU  172      51.870  56.411 -16.463  1.00  0.00      A3
ATOM  1319  CA LEU  172      53.550  57.133 -17.496  1.00 86.02      A3
ATOM  1320  CB LEU  172      53.500  58.357 -16.607  1.00 86.31      A3
ATOM  1321  CG LEU  172      54.022  59.658 -17.203  1.00 87.48      A3
ATOM  1322  CD1 LEU  172      53.436  59.939 -18.596  1.00 87.68      A3
ATOM  1323  CD2 LEU  172      53.645  60.778 -16.251  1.00 87.95      A3
ATOM  1324  C  LEU  172      54.813  56.357 -17.180  1.00 85.92      A3
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FIGURE 5

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ATOM 1325 O  LEU 172    55.896 56.660 -17.692 1.00 86.23    A3
ATOM 1326 N  ALA 173    54.733 55.383 -16.282 1.00 85.49    A3
ATOM 1327 H  ALA 173    53.899 55.276 -15.769 1.00  0.00    A3
ATOM 1328 CA ALA 173    55.856 54.497 -16.087 1.00 85.65    A3
ATOM 1329 CB ALA 173    56.602 54.859 -14.809 1.00 85.01    A3
ATOM 1330 C  ALA 173    55.330 53.073 -16.008 1.00 86.54    A3
ATOM 1331 OT1 ALA 173    55.585 52.347 -16.971 1.00 87.21    A3
ATOM 1332 OT2 ALA 173    54.650 52.707 -15.036 1.00 87.31    A3
ATOM 1333 CB LEU 210    45.234 42.591 25.453 1.00 52.47    B1
ATOM 1334 CG LEU 210    43.799 42.058 25.547 1.00 51.68    B1
ATOM 1335 CD1 LEU 210    43.123 42.562 26.804 1.00 53.37    B1
ATOM 1336 CD2 LEU 210    43.050 42.453 24.303 1.00 51.37    B1
ATOM 1337 C  LEU 210    46.770 44.374 24.596 1.00 50.98    B1
ATOM 1338 O  LEU 210    46.475 45.267 23.790 1.00 51.76    B1
ATOM 1339 HT1 LEU 210    44.382 44.922 24.421 1.00  0.00    B1
ATOM 1340 HT2 LEU 210    45.157 45.974 25.414 1.00  0.00    B1
ATOM 1341 N  LEU 210    44.705 45.041 25.406 1.00 53.59    B1
ATOM 1342 HT3 LEU 210    43.855 45.012 25.997 1.00  0.00    B1
ATOM 1343 CA LEU 210    45.730 44.038 25.676 1.00 52.35    B1
ATOM 1344 N  PRO 211    47.974 43.825 24.494 1.00 49.35    B1
ATOM 1345 CD PRO 211    48.621 43.024 25.532 1.00 49.52    B1
ATOM 1346 CA PRO 211    48.895 44.191 23.419 1.00 49.04    B1
ATOM 1347 CB PRO 211    50.209 43.571 23.865 1.00 49.02    B1
ATOM 1348 CG PRO 211    49.794 42.438 24.783 1.00 49.77    B1
ATOM 1349 C  PRO 211    48.543 43.864 21.965 1.00 48.03    B1
ATOM 1350 O  PRO 211    47.872 42.896 21.622 1.00 49.05    B1
ATOM 1351 N  GLN 212    49.032 44.675 21.051 1.00 46.52    B1
ATOM 1352 H  GLN 212    49.506 45.478 21.349 1.00  0.00    B1
ATOM 1353 CA GLN 212    48.839 44.461 19.641 1.00 45.47    B1
ATOM 1354 CB GLN 212    49.533 45.522 18.849 1.00 46.81    B1
ATOM 1355 CG GLN 212    48.482 46.139 17.999 1.00 49.55    B1
ATOM 1356 CD GLN 212    49.024 46.703 16.709 1.00 54.21    B1
ATOM 1357 OE1 GLN 212    48.429 47.672 16.232 1.00 57.72    B1
ATOM 1358 NE2 GLN 212    50.086 46.176 16.074 1.00 52.39    B1
ATOM 1359 HE21 GLN 212    50.530 45.383 16.430 1.00  0.00    B1
ATOM 1360 HE22 GLN 212    50.341 46.625 15.244 1.00  0.00    B1
ATOM 1361 C  GLN 212    49.390 43.133 19.185 1.00 44.79    B1
ATOM 1362 O  GLN 212    48.959 42.520 18.208 1.00 44.01    B1
ATOM 1363 N  SER 213    50.401 42.671 19.893 1.00 44.72    B1
ATOM 1364 H  SER 213    50.730 43.115 20.698 1.00  0.00    B1
ATOM 1365 CA SER 213    51.025 41.424 19.521 1.00 43.76    B1
ATOM 1366 CB SER 213    52.220 41.124 20.354 1.00 45.29    B1
ATOM 1367 OG SER 213    51.802 41.455 21.681 1.00 52.50    B1
ATOM 1368 HG SER 213    52.479 41.127 22.288 1.00  0.00    B1
ATOM 1369 C  SER 213    50.014 40.376 19.784 1.00 40.92    B1
ATOM 1370 O  SER 213    49.964 39.492 18.947 1.00 43.32    B1
ATOM 1371 N  PHE 214    49.242 40.571 20.876 1.00 38.86    B1
ATOM 1372 H  PHE 214    49.414 41.370 21.410 1.00  0.00    B1
ATOM 1373 CA PHE 214    48.210 39.664 21.336 1.00 37.40    B1
ATOM 1374 CB PHE 214    47.568 40.064 22.634 1.00 37.45    B1
ATOM 1375 CG PHE 214    46.494 39.080 23.035 1.00 41.01    B1
ATOM 1376 CD1 PHE 214    45.176 39.459 23.044 1.00 42.77    B1
ATOM 1377 CD2 PHE 214    46.818 37.794 23.400 1.00 42.02    B1
ATOM 1378 CE1 PHE 214    44.197 38.554 23.423 1.00 41.82    B1
ATOM 1379 CE2 PHE 214    45.834 36.898 23.776 1.00 41.70    B1
ATOM 1380 CZ PHE 214    44.519 37.277 23.791 1.00 41.05    B1
ATOM 1381 C  PHE 214    47.109 39.656 20.321 1.00 36.54    B1
ATOM 1382 O  PHE 214    46.735 38.566 19.889 1.00 37.99    B1
ATOM 1383 N  LEU 215    46.616 40.812 19.893 1.00 33.27    B1
ATOM 1384 H  LEU 215    47.008 41.642 20.238 1.00  0.00    B1
ATOM 1385 CA LEU 215    45.504 40.864 18.966 1.00 30.38    B1
ATOM 1386 CB LEU 215    45.099 42.282 18.701 1.00 31.82    B1
ATOM 1387 CG LEU 215    43.857 42.530 17.893 1.00 32.78    B1
ATOM 1388 CD1 LEU 215    42.727 41.963 18.737 1.00 32.95    B1
ATOM 1389 CD2 LEU 215    43.688 44.011 17.508 1.00 28.93    B1
ATOM 1390 C  LEU 215    45.811 40.232 17.648 1.00 29.57    B1
ATOM 1391 O  LEU 215    44.922 39.632 17.055 1.00 31.28    B1
ATOM 1392 N  LEU 216    47.031 40.379 17.155 1.00 29.44    B1
ATOM 1393 H  LEU 216    47.677 40.935 17.646 1.00  0.00    B1
ATOM 1394 CA LEU 216    47.465 39.790 15.893 1.00 29.89    B1
ATOM 1395 CB LEU 216    48.791 40.450 15.472 1.00 28.61    B1
ATOM 1396 CG LEU 216    48.682 41.877 14.939 1.00 26.84    B1
ATOM 1397 CD1 LEU 216    49.925 42.558 15.344 1.00 28.57    B1
ATOM 1398 CD2 LEU 216    48.446 41.950 13.452 1.00 24.09    B1
ATOM 1399 C  LEU 216    47.613 38.274 16.062 1.00 31.23    B1
ATOM 1400 O  LEU 216    47.328 37.514 15.138 1.00 29.20    B1
ATOM 1401 N  LYS 217    47.999 37.826 17.261 1.00 32.50    B1
ATOM 1402 H  LYS 217    48.305 38.482 17.926 1.00  0.00    B1
ATOM 1403 CA LYS 217    48.067 36.439 17.599 1.00 34.90    B1
ATOM 1404 CB LYS 217    48.645 36.280 19.002 1.00 38.07    B1
ATOM 1405 CG LYS 217    49.394 34.978 19.109 1.00 45.25    B1
ATOM 1406 CD LYS 217    49.714 34.491 20.521 1.00 53.27    B1
ATOM 1407 CE LYS 217    50.229 33.024 20.297 1.00 59.03    B1
ATOM 1408 NZ LYS 217    50.213 32.135 21.467 1.00 62.10    B1
ATOM 1409 HZ1 LYS 217    49.239 32.056 21.824 1.00  0.00    B1
ATOM 1410 HZ2 LYS 217    50.830 32.515 22.214 1.00  0.00    B1
ATOM 1411 HZ3 LYS 217    50.554 31.195 21.179 1.00  0.00    B1
ATOM 1412 C  LYS 217    46.617 35.950 17.546 1.00 36.77    B1
ATOM 1413 O  LYS 217    46.311 34.933 16.886 1.00 39.58    B1
ATOM 1414 N  CYS 218    45.664 36.638 18.177 1.00 34.86    B1
ATOM 1415 H  CYS 218    45.907 37.388 18.751 1.00  0.00    B1
ATOM 1416 CA CYS 218    44.277 36.238 18.076 1.00 33.61    B1
ATOM 1417 CB CYS 218    43.430 37.175 18.846 1.00 33.21    B1
ATOM 1418 SG CYS 218    43.856 36.710 20.515 1.00 35.92    B1
ATOM 1419 C  CYS 218    43.766 36.189 16.652 1.00 32.89    B1
ATOM 1420 O  CYS 218    43.155 35.169 16.323 1.00 34.71    B1
ATOM 1421 N  LEU 219    44.035 37.169 15.777 1.00 29.52    B1
ATOM 1422 H  LEU 219    44.512 37.960 16.104 1.00  0.00    B1
ATOM 1423 CA LEU 219    43.614 37.119 14.393 1.00 27.44    B1
ATOM 1424 CB LEU 219    44.116 38.412 13.727 1.00 26.24    B1
ATOM 1425 CG LEU 219    43.884 38.768 12.241 1.00 25.07    B1
ATOM 1426 CD1 LEU 219    42.402 38.975 11.996 1.00 26.24    B1
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FIGURE 5

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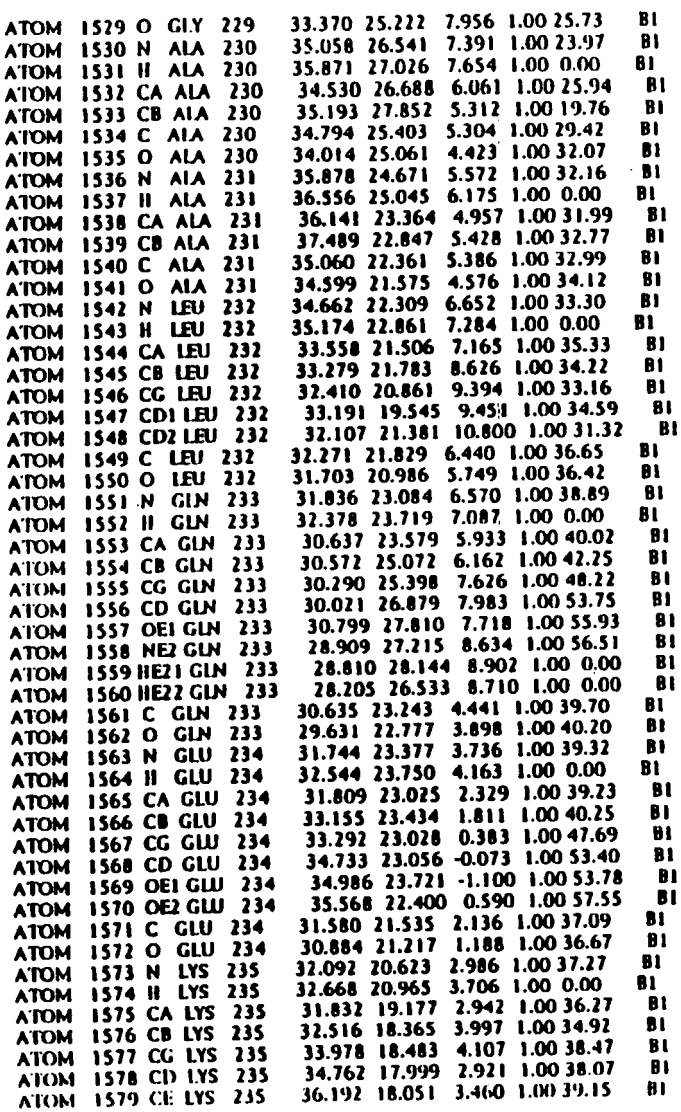
ATOM  1427 CD2 LEU  219      44.563  [illegible]51  11.882  1.00 22.10      B1
ATOM  1428 C   LEU  219      44.121  35.867  13.634  1.00 28.24      B1
ATOM  1429 O   LEU  219      43.373  35.204  12.889  1.00 27.12      B1
ATOM  1430 N   GLU  220      45.399  35.499  13.795  1.00 28.06      B1
ATOM  1431 H   GLU  220      45.957  35.974  14.448  1.00  0.00      B1
ATOM  1432 CA  GLU  220      45.963  34.411  13.048  1.00 28.38      B1
ATOM  1433 CB  GLU  220      47.376  34.198  13.469  1.00 34.25      B1
ATOM  1434 CG  GLU  220      48.049  33.079  12.666  1.00 46.36      B1
ATOM  1435 CD  GLU  220      49.545  32.794  12.907  1.00 55.51      B1
ATOM  1436 OE1 GLU  220      50.113  32.133  12.021  1.00 58.95      B1
ATOM  1437 OE2 GLU  220      50.144  33.213  13.930  1.00 60.41      B1
ATOM  1438 C   GLU  220      45.134  33.193  13.354  1.00 27.30      B1
ATOM  1439 O   GLU  220      44.662  32.524  12.437  1.00 27.08      B1
ATOM  1440 N   GLN  221      44.866  33.023  14.642  1.00 25.42      B1
ATOM  1441 H   GLN  221      45.229  33.687  15.268  1.00  0.00      B1
ATOM  1442 CA  GLN  221      44.074  31.940  15.176  1.00 26.28      B1
ATOM  1443 CB  GLN  221      44.143  31.927  16.691  1.00 26.78      B1
ATOM  1444 CG  GLN  221      45.555  31.456  17.011  1.00 29.19      B1
ATOM  1445 CD  GLN  221      45.752  31.067  18.442  1.00 31.98      B1
ATOM  1446 OE1 GLN  221      46.472  30.162  18.808  1.00 35.98      B1
ATOM  1447 NE2 GLN  221      45.110  31.736  19.347  1.00 39.31      B1
ATOM  1448 HE21 GLN  221      45.263  31.423  20.246  1.00  0.00      B1
ATOM  1449 HE22 GLN  221      44.571  32.514  19.111  1.00  0.00      H1
ATOM  1450 C   GLN  221      42.615  31.925  14.789  1.00 26.21      B1
ATOM  1451 O   GLN  221      42.186  30.896  14.269  1.00 30.69      B1
ATOM  1452 N   VAL  222      41.814  32.962  14.984  1.00 23.63      B1
ATOM  1453 H   VAL  222      42.199  33.746  15.426  1.00  0.00      B1
ATOM  1454 CA  VAL  222      40.429  33.034  14.537  1.00 21.92      B1
ATOM  1455 CB  VAL  222      39.934  34.442  14.793  1.00 21.36      B1
ATOM  1456 CG1 VAL  222      38.706  34.831  14.027  1.00 17.72      B1
ATOM  1457 CG2 VAL  222      39.671  34.496  16.257  1.00 20.95      B1
ATOM  1458 C   VAL  222      40.374  32.707  13.066  1.00 22.65      B1
ATOM  1459 O   VAL  222      39.475  32.013  12.632  1.00 23.72      B1
ATOM  1460 N   ARG  223      41.341  33.120  12.283  1.00 23.95      B1
ATOM  1461 H   ARG  223      42.099  33.614  12.666  1.00  0.00      B1
ATOM  1462 CA  ARG  223      41.309  32.939  10.844  1.00 27.19      B1
ATOM  1463 CB  ARG  223      42.294  33.935  10.283  1.00 29.26      B1
ATOM  1464 CG  ARG  223      42.102  34.364   8.869  1.00 35.23      B1
ATOM  1465 CD  ARG  223      42.880  33.487   7.929  1.00 41.88      B1
ATOM  1466 NE  ARG  223      41.972  32.676   7.096  1.00 47.42      B1
ATOM  1467 HE  ARG  223      41.451  31.953   7.502  1.00  0.00      B1
ATOM  1468 CZ  ARG  223      41.875  32.896   5.784  1.00 46.15      B1
ATOM  1469 NH1 ARG  223      42.575  33.837   5.246  1.00 49.54      B1
ATOM  1470 HH11 ARG  223      42.522  33.989   4.259  1.00  0.00      B1
ATOM  1471 HH12 ARG  223      43.156  34.428   5.805  1.00  0.00      B1
ATOM  1472 NH2 ARG  223      41.178  32.161   4.952  1.00 45.74      B1
ATOM  1473 HH21 ARG  223      40.697  31.353   5.290  1.00  0.00      B1
ATOM  1474 HH22 ARG  223      41.154  32.399   3.980  1.00  0.00      B1
ATOM  1475 C   ARG  223      41.624  31.492  10.430  1.00 29.13      B1
ATOM  1476 O   ARG  223      41.181  30.987   9.376  1.00 29.32      B1
ATOM  1477 N   LYS  224      42.413  30.791  11.259  1.00 29.17      B1
ATOM  1478     LYS  224      42.791  31.235  12.048  1.00  0.00      H1
ATOM  1479 CA  LYS  224      42.714  29.411  10.994  1.00 27.70      B1
ATOM  1480 CB  LYS  224      43.922  29.085  11.818  1.00 30.07      B1
ATOM  1481 CG  LYS  224      44.372  27.660  11.706  1.00 36.70      B1
ATOM  1482 CD  LYS  224      45.829  27.544  12.127  1.00 41.68      B1
ATOM  1483 CE  LYS  224      46.303  26.478  11.131  1.00 48.18      B1
ATOM  1484 NZ  LYS  224      47.750  26.492  10.913  1.00 53.57      B1
ATOM  1485 HZ1 LYS  224      48.230  26.241  11.801  1.00  0.00      H1
ATOM  1486 HZ2 LYS  224      48.057  27.436  10.606  1.00  0.00      H1
ATOM  1487 HZ3 LYS  224      47.998  25.792  10.183  1.00  0.00      H1
ATOM  1488 C   LYS  224      41.464  28.598  11.347  1.00 26.27      B1
ATOM  1489 O   LYS  224      40.970  27.810  10.510  1.00 24.82      B1
ATOM  1490 N   ILE  225      40.892  28.835  12.547  1.00 24.75      B1
ATOM  1491 H   ILE  225      41.308  29.487  13.151  1.00  0.00      H1
ATOM  1492 CA  ILE  225      39.656  28.147  12.943  1.00 23.33      B1
ATOM  1493 CB  ILE  225      39.146  28.622  14.296  1.00 18.08      B1
ATOM  1494 CG2 ILE  225      37.874  27.872  14.577  1.00 15.43      B1
ATOM  1495 CG1 ILE  225      40.161  28.400  15.380  1.00 13.38      B1
ATOM  1496 CD  ILE  225      39.787  28.967  16.749  1.00 13.59      B1
ATOM  1497 C   ILE  225      38.594  28.437  11.889  1.00 27.28      B1
ATOM  1498 O   ILE  225      37.978  27.492  11.400  1.00 31.49      B1
ATOM  1499 N   GLN  226      38.396  29.677  11.402  1.00 29.69      B1
ATOM  1500 H   GLN  226      38.894  30.413  11.803  1.00  0.00      H1
ATOM  1501 CA  GLN  226      37.450  29.969  10.313  1.00 29.12      B1
ATOM  1502 CB  GLN  226      37.366  31.438   9.962  1.00 32.26      B1
ATOM  1503 CG  GLN  226      36.682  32.156  11.108  1.00 36.28      B1
ATOM  1504 CD  GLN  226      36.429  33.613  10.816  1.00 37.88      B1
ATOM  1505 OE1 GLN  226      37.158  34.281  10.076  1.00 36.34      B1
ATOM  1506 NE2 GLN  226      35.359  34.114  11.421  1.00 39.62      B1
ATOM  1507 HE21 GLN  226      34.823  33.501  11.971  1.00  0.00      H1
ATOM  1508 HE22 GLN  226      35.153  35.057  11.287  1.00  0.00      H1
ATOM  1509 C   GLN  226      37.714  29.295   9.007  1.00 26.82      B1
ATOM  1510 O   GLN  226      36.775  28.887   8.325  1.00 27.45      B1
ATOM  1511 N   GLY  227      38.940  29.186   8.570  1.00 26.55      B1
ATOM  1512 H   GLY  227      39.688  29.612   9.043  1.00  0.00      H1
ATOM  1513 CA  GLY  227      39.195  28.427   7.348  1.00 27.27      B1
ATOM  1514 C   GLY  227      38.832  26.949   7.574  1.00 27.65      B1
ATOM  1515 O   GLY  227      38.287  26.291   6.656  1.00 26.79      B1
ATOM  1516 N   ASP  228      39.025  26.429   8.819  1.00 27.03      B1
ATOM  1517 H   ASP  228      39.460  26.957   9.523  1.00  0.00      H1
ATOM  1518 CA  ASP  228      38.618  25.038   9.052  1.00 28.20      B1
ATOM  1519 CB  ASP  228      38.986  24.492  10.391  1.00 26.04      B1
ATOM  1520 CG  ASP  228      40.427  24.554  10.774  1.00 24.88      B1
ATOM  1521 OD1 ASP  228      40.627  24.521  11.977  1.00 23.57      B1
ATOM  1522 OD2 ASP  228      41.302  24.637   9.912  1.00 23.32      B1
ATOM  1523 C   ASP  228      37.120  24.830   8.992  1.00 27.23      B1
ATOM  1524 O   ASP  228      36.662  23.900   8.336  1.00 27.07      B1
ATOM  1525 N   GLY  229      36.390  25.739   9.639  1.00 26.74      B1
ATOM  1526 H   GLY  229      36.861  26.444  10.134  1.00  0.00      H1
ATOM  1527 CA  GLY  229      34.946  25.723   9.673  1.00 25.87      B1
ATOM  1528 C   GLY  229      34.393  25.825   8.274  1.00 24.95      B1
```

FIGURE 5



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ATOM  1529 O   GLY  229     33.370  25.222   7.956  1.00 25.73      B1
ATOM  1530 N   ALA  230     35.058  26.541   7.391  1.00 23.97      B1
ATOM  1531 H   ALA  230     35.871  27.026   7.654  1.00  0.00      B1
ATOM  1532 CA  ALA  230     34.530  26.688   6.061  1.00 25.94      B1
ATOM  1533 CB  ALA  230     35.193  27.852   5.312  1.00 19.76      B1
ATOM  1534 C   ALA  230     34.794  25.403   5.304  1.00 29.42      B1
ATOM  1535 O   ALA  230     34.014  25.061   4.423  1.00 32.07      B1
ATOM  1536 N   ALA  231     35.878  24.671   5.572  1.00 32.16      B1
ATOM  1537 H   ALA  231     36.556  25.045   6.175  1.00  0.00      B1
ATOM  1538 CA  ALA  231     36.141  23.364   4.957  1.00 31.99      B1
ATOM  1539 CB  ALA  231     37.489  22.847   5.428  1.00 32.77      B1
ATOM  1540 C   ALA  231     35.060  22.361   5.386  1.00 32.99      B1
ATOM  1541 O   ALA  231     34.599  21.575   4.576  1.00 34.12      B1
ATOM  1542 N   LEU  232     34.662  22.309   6.652  1.00 33.30      B1
ATOM  1543 H   LEU  232     35.174  22.861   7.284  1.00  0.00      B1
ATOM  1544 CA  LEU  232     33.558  21.506   7.165  1.00 35.33      B1
ATOM  1545 CB  LEU  232     33.279  21.783   8.626  1.00 34.22      B1
ATOM  1546 CG  LEU  232     32.410  20.861   9.394  1.00 33.16      B1
ATOM  1547 CD1 LEU  232     33.191  19.545   9.458  1.00 34.59      B1
ATOM  1548 CD2 LEU  232     32.107  21.381  10.800  1.00 31.32      B1
ATOM  1549 C   LEU  232     32.271  21.829   6.440  1.00 36.65      B1
ATOM  1550 O   LEU  232     31.703  20.986   5.749  1.00 36.42      B1
ATOM  1551 N   GLN  233     31.836  23.084   6.570  1.00 38.89      B1
ATOM  1552 H   GLN  233     32.378  23.719   7.087  1.00  0.00      B1
ATOM  1553 CA  GLN  233     30.637  23.579   5.933  1.00 40.02      B1
ATOM  1554 CB  GLN  233     30.572  25.072   6.162  1.00 42.25      B1
ATOM  1555 CG  GLN  233     30.290  25.398   7.626  1.00 48.22      B1
ATOM  1556 CD  GLN  233     30.021  26.879   7.983  1.00 53.75      B1
ATOM  1557 OE1 GLN  233     30.799  27.810   7.718  1.00 55.93      B1
ATOM  1558 NE2 GLN  233     28.909  27.215   8.634  1.00 56.51      B1
ATOM  1559 HE21 GLN  233     28.810  28.144   8.902  1.00  0.00      B1
ATOM  1560 HE22 GLN  233     28.205  26.533   8.710  1.00  0.00      B1
ATOM  1561 C   GLN  233     30.635  23.243   4.441  1.00 39.70      B1
ATOM  1562 O   GLN  233     29.631  22.777   3.898  1.00 40.20      B1
ATOM  1563 N   GLU  234     31.744  23.377   3.736  1.00 39.32      B1
ATOM  1564 H   GLU  234     32.544  23.750   4.163  1.00  0.00      B1
ATOM  1565 CA  GLU  234     31.809  23.025   2.329  1.00 39.23      B1
ATOM  1566 CB  GLU  234     33.155  23.434   1.811  1.00 40.25      B1
ATOM  1567 CG  GLU  234     33.292  23.028   0.383  1.00 47.69      B1
ATOM  1568 CD  GLU  234     34.733  23.056  -0.073  1.00 53.40      B1
ATOM  1569 OE1 GLU  234     34.986  23.721  -1.100  1.00 53.78      B1
ATOM  1570 OE2 GLU  234     35.568  22.400   0.590  1.00 57.55      B1
ATOM  1571 C   GLU  234     31.580  21.535   2.136  1.00 37.09      B1
ATOM  1572 O   GLU  234     30.884  21.217   1.188  1.00 36.67      B1
ATOM  1573 N   LYS  235     32.092  20.623   2.986  1.00 37.27      B1
ATOM  1574 H   LYS  235     32.668  20.965   3.706  1.00  0.00      B1
ATOM  1575 CA  LYS  235     31.832  19.177   2.942  1.00 36.27      B1
ATOM  1576 CB  LYS  235     32.516  18.365   3.997  1.00 34.92      B1
ATOM  1577 CG  LYS  235     33.978  18.483   4.107  1.00 38.47      B1
ATOM  1578 CD  LYS  235     34.762  17.999   2.921  1.00 38.07      B1
ATOM  1579 CE  LYS  235     36.192  18.051   3.460  1.00 39.15      B1
ATOM  1580 NZ  LYS  235     37.117  17.460   2.521  1.00 41.34      B1
ATOM  1581 HZ1 LYS  235     37.080  17.978   1.622  1.00  0.00      B1
ATOM  1582 HZ2 LYS  235     36.854  16.466   2.363  1.00  0.00      B1
ATOM  1583 HZ3 LYS  235     38.080  17.497   2.911  1.00  0.00      B1
ATOM  1584 C   LYS  235     30.363  18.847   3.204  1.00 35.20      B1
ATOM  1585 O   LYS  235     29.722  18.102   2.463  1.00 35.60      B1
ATOM  1586 N   LEU  236     29.807  19.332   4.301  1.00 33.53      B1
ATOM  1587 H   LEU  236     30.363  19.888   4.885  1.00  0.00      B1
ATOM  1588 CA  LEU  236     28.417  19.116   4.641  1.00 32.30      B1
ATOM  1589 CB  LEU  236     28.093  19.918   5.894  1.00 28.65      B1
ATOM  1590 CG  LEU  236     28.791  19.441   7.148  1.00 28.23      B1
ATOM  1591 CD1 LEU  236     28.703  20.460   8.268  1.00 24.14      B1
ATOM  1592 CD2 LEU  236     28.132  18.163   7.587  1.00 26.66      B1
ATOM  1593 C   LEU  236     27.590  19.574   3.453  1.00 33.09      B1
ATOM  1594 O   LEU  236     26.691  18.849   3.064  1.00 35.13      B1
ATOM  1595 N   CYS  237     27.870  20.670   2.753  1.00 34.49      B1
ATOM  1596 H   CYS  237     28.611  21.251   3.025  1.00  0.00      B1
ATOM  1597 CA  CYS  237     27.064  21.016   1.606  1.00 34.95      B1
ATOM  1598 C   CYS  237     27.324  20.090   0.451  1.00 35.97      B1
ATOM  1599 O   CYS  237     26.360  19.573  -0.089  1.00 36.09      B1
ATOM  1600 CB  CYS  237     27.334  22.413   1.130  1.00 35.18      B1
ATOM  1601 SG  CYS  237     26.409  22.880  -0.365  1.00 36.40      B1
ATOM  1602 N   ALA  238     28.571  19.804   0.074  1.00 37.29      B1
ATOM  1603 H   ALA  238     29.324  20.158   0.591  1.00  0.00      B1
ATOM  1604 CA  ALA  238     28.841  18.973  -1.090  1.00 36.80      B1
ATOM  1605 CB  ALA  238     30.274  18.684  -1.403  1.00 37.35      B1
ATOM  1606 C   ALA  238     28.320  17.617  -0.911  1.00 36.49      B1
ATOM  1607 O   ALA  238     27.645  17.198  -1.809  1.00 36.54      B1
ATOM  1608 N   THR  239     28.628  16.969   0.193  1.00 38.80      B1
ATOM  1609 H   THR  239     29.236  17.391   0.821  1.00  0.00      B1
ATOM  1610 CA  THR  239     28.230  15.587   0.464  1.00 41.31      B1
ATOM  1611 CB  THR  239     29.158  15.035   1.554  1.00 42.38      B1
ATOM  1612 OG1 THR  239     30.473  15.265   1.031  1.00 45.70      B1
ATOM  1613 HG1 THR  239     31.019  15.668   1.709  1.00  0.00      B1
ATOM  1614 CG2 THR  239     28.936  13.574   1.916  1.00 41.85      B1
ATOM  1615 C   THR  239     26.771  15.341   0.864  1.00 41.94      B1
ATOM  1616 O   THR  239     26.260  14.284   0.460  1.00 43.54      B1
ATOM  1617 N   TYR  240     26.095  16.207   1.669  1.00 40.07      B1
ATOM  1618 H   TYR  240     26.538  17.034   1.953  1.00  0.00      B1
ATOM  1619 CA  TYR  240     24.718  15.992   2.084  1.00 38.21      B1
ATOM  1620 CB  TYR  240     24.594  15.993   3.618  1.00 38.08      B1
ATOM  1621 CG  TYR  240     25.524  14.926   4.193  1.00 43.37      B1
ATOM  1622 CD1 TYR  240     26.475  15.243   5.149  1.00 45.06      B1
ATOM  1623 CE1 TYR  240     27.420  14.283   5.529  1.00 47.35      B1
ATOM  1624 CD2 TYR  240     25.518  13.643   3.641  1.00 43.89      B1
ATOM  1625 CE2 TYR  240     26.442  12.690   4.003  1.00 44.77      B1
ATOM  1626 CZ  TYR  240     27.410  13.005   4.943  1.00 47.96      B1
ATOM  1627 OH  TYR  240     28.390  12.047   5.244  1.00 46.59      B1
ATOM  1628 HH  TYR  240     28.027  11.187   4.992  1.00  0.00      B1
ATOM  1629 C   TYR  240     23.781  17.032   1.516  1.00 39.49      B1
ATOM  1630 O   TYR  240     22.587  16.934   1.775  1.00 42.76      B1
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FIGURE 5

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ATOM  1631  N   LYS  241     24.174  18.[illegible]  0.694  1.00 37.36      B1
ATOM  1632  H   LYS  241     25.091  18.023  0.345  1.00  0.00      B1
ATOM  1633  CA  LYS  241     23.314  19.115  0.275  1.00 36.37      B1
ATOM  1634  CB  LYS  241     22.173  18.648 -0.595  1.00 38.38      B1
ATOM  1635  CG  LYS  241     22.645  17.940 -1.838  1.00 42.94      B1
ATOM  1636  CD  LYS  241     23.468  18.809 -2.737  1.00 46.97      B1
ATOM  1637  CE  LYS  241     23.657  18.070 -4.051  1.00 49.20      B1
ATOM  1638  NZ  LYS  241     22.509  18.372 -4.893  1.00 51.54      B1
ATOM  1639  HZ1 LYS  241     22.447  19.400 -5.038  1.00  0.00      B1
ATOM  1640  HZ2 LYS  241     21.641  18.041 -4.426  1.00  0.00      B1
ATOM  1641  HZ3 LYS  241     22.609  17.895 -5.811  1.00  0.00      B1
ATOM  1642  C   LYS  241     22.720  19.904  1.429  1.00 33.37      B1
ATOM  1643  O   LYS  241     21.728  20.580  1.223  1.00 33.90      B1
ATOM  1644  N   LEU  242     23.286  19.853  2.648  1.00 31.40      B1
ATOM  1645  H   LEU  242     24.055  19.260  2.756  1.00  0.00      B1
ATOM  1646  CA  LEU  242     22.904  20.682  3.758  1.00 31.09      B1
ATOM  1647  CB  LEU  242     23.253  20.059  5.096  1.00 28.55      B1
ATOM  1648  CG  LEU  242     22.571  18.798  5.641  1.00 30.36      B1
ATOM  1649  CD1 LEU  242     22.530  18.814  7.138  1.00 29.62      B1
ATOM  1650  CD2 LEU  242     21.086  18.861  5.443  1.00 31.94      B1
ATOM  1651  C   LEU  242     23.778  21.933  3.550  1.00 34.03      B1
ATOM  1652  O   LEU  242     24.903  22.027  4.058  1.00 35.53      B1
ATOM  1653  N   CYS  243     23.316  22.883  2.722  1.00 34.89      B1
ATOM  1654  H   CYS  243     22.491  22.665  2.238  1.00  0.00      B1
ATOM  1655  CA  CYS  243     24.051  24.083  2.377  1.00 35.42      B1
ATOM  1656  C   CYS  243     23.492  25.335  2.975  1.00 36.85      B1
ATOM  1657  O   CYS  243     23.956  26.400  2.565  1.00 40.10      B1
ATOM  1658  CB  CYS  243     24.046  24.383  0.929  1.00 33.12      B1
ATOM  1659  SG  CYS  243     24.438  22.883  0.099  1.00 38.25      B1
ATOM  1660  N   HIS  244     22.496  25.393  3.848  1.00 35.37      B1
ATOM  1661  H   HIS  244     22.185  24.588  4.318  1.00  0.00      B1
ATOM  1662  CA  HIS  244     21.939  26.676  4.191  1.00 33.29      B1
ATOM  1663  CB  HIS  244     20.655  26.987  3.340  1.00 33.64      B1
ATOM  1664  CG  HIS  244     20.915  27.205  1.857  1.00 33.12      B1
ATOM  1665  CD2 HIS  244     20.288  26.584  0.814  1.00 37.29      B1
ATOM  1666  ND1 HIS  244     21.874  27.902  1.298  1.00 36.85      B1
ATOM  1667  HD1 HIS  244     22.648  28.281  1.778  1.00  0.00      B1
ATOM  1668  CE1 HIS  244     21.874  27.722 -0.013  1.00 35.95      B1
ATOM  1669  NE2 HIS  244     20.910  26.920 -0.301  1.00 35.54      B1
ATOM  1670  HE2 HIS  244     20.616  26.706 -1.214  1.00  0.00      B1
ATOM  1671  C   HIS  244     21.621  26.565  5.650  1.00 33.38      B1
ATOM  1672  O   HIS  244     20.546  26.105  6.029  1.00 33.23      B1
ATOM  1673  N   PRO  245     22.539  27.018  6.499  1.00 33.21      B1
ATOM  1674  CD  PRO  245     23.851  27.524  6.099  1.00 31.29      B1
ATOM  1675  CA  PRO  245     22.373  26.979  7.948  1.00 34.16      B1
ATOM  1676  CB  PRO  245     23.490  27.799  8.467  1.00 32.85      B1
ATOM  1677  CG  PRO  245     24.564  27.549  7.428  1.00 31.74      B1
ATOM  1678  C   PRO  245     21.032  27.470  8.407  1.00 36.26      B1
ATOM  1679  O   PRO  245     20.478  26.878  9.315  1.00 38.13      B1
ATOM  1680  N   GLU  246     20.529  28.463  7.640  1.00 39.64      B1
ATOM  1681  H   GLU  246     21.134  28.747  6.934  1.00  0.00      B1
ATOM  1682  C   GLU  246     19.257  29.229  7.711  1.00 41.10      B1
ATOM  1683  CB  GLU  246     19.044  30.107  6.438  1.00 44.15      B1
ATOM  1684  CG  GLU  246     20.256  30.918  5.944  1.00 47.07      B1
ATOM  1685  CD  GLU  246     20.813  30.539  4.558  1.00 52.63      B1
ATOM  1686  OE1 GLU  246     22.054  30.545  4.374  1.00 54.22      B1
ATOM  1687  OE2 GLU  246     20.002  30.250  3.656  1.00 54.39      B1
ATOM  1688  C   GLU  246     18.071  28.298  7.819  1.00 40.57      B1
ATOM  1689  O   GLU  246     17.308  28.338  8.791  1.00 39.90      B1
ATOM  1690  N   GLU  247     18.025  27.388  6.840  1.00 40.32      B1
ATOM  1691  H   GLU  247     18.750  27.334  6.190  1.00  0.00      B1
ATOM  1692  CA  GLU  247     17.001  26.347  6.830  1.00 40.76      B1
ATOM  1693  CB  GLU  247     17.139  25.423  5.642  1.00 44.03      B1
ATOM  1694  CG  GLU  247     16.830  26.240  4.400  1.00 48.54      B1
ATOM  1695  CD  GLU  247     17.163  25.628  3.050  1.00 50.24      B1
ATOM  1696  OE1 GLU  247     16.849  26.299  2.056  1.00 52.92      B1
ATOM  1697  OE2 GLU  247     17.744  24.533  2.987  1.00 50.84      B1
ATOM  1698  C   GLU  247     16.966  25.444  8.034  1.00 39.24      B1
ATOM  1699  O   GLU  247     15.915  24.888  8.329  1.00 39.40      B1
ATOM  1700  N   LEU  248     18.066  25.280  8.760  1.00 37.92      B1
ATOM  1701  H   LEU  248     18.864  25.814  8.576  1.00  0.00      B1
ATOM  1702  CA  LEU  248     18.101  24.338  9.858  1.00 35.75      B1
ATOM  1703  CB  LEU  248     19.458  23.623  9.796  1.00 34.13      B1
ATOM  1704  CG  LEU  248     19.669  22.866  8.430  1.00 34.00      B1
ATOM  1705  CD1 LEU  248     20.997  22.149  8.306  1.00 33.97      B1
ATOM  1706  CD2 LEU  248     18.620  21.810  8.322  1.00 32.33      B1
ATOM  1707  C   LEU  248     17.871  25.031 11.155  1.00 36.51      B1
ATOM  1708  O   LEU  248     17.736  24.370 12.186  1.00 36.31      B1
ATOM  1709  N   VAL  249     17.663  26.350 11.146  1.00 38.88      B1
ATOM  1710  H   VAL  249     17.566  26.810 10.283  1.00  0.00      B1
ATOM  1711  CA  VAL  249     17.573  27.133 12.371  1.00 41.39      B1
ATOM  1712  CB  VAL  249     17.265  28.640 12.020  1.00 43.72      B1
ATOM  1713  CG1 VAL  249     15.804  28.985 11.776  1.00 44.70      B1
ATOM  1714  CG2 VAL  249     17.702  29.434 13.214  1.00 45.20      B1
ATOM  1715  C   VAL  249     16.590  26.635 13.406  1.00 42.61      B1
ATOM  1716  O   VAL  249     16.912  26.716 14.594  1.00 44.77      B1
ATOM  1717  N   LEU  250     15.453  26.035 13.016  1.00 43.61      B1
ATOM  1718  H   LEU  250     15.319  25.919 12.053  1.00  0.00      B1
ATOM  1719  CA  LEU  250     14.457  25.537 13.987  1.00 43.96      B1
ATOM  1720  CB  LEU  250     13.102  25.296 13.373  1.00 44.88      B1
ATOM  1721  CG  LEU  250     12.729  26.281 12.313  1.00 47.04      B1
ATOM  1722  CD1 LEU  250     13.092  25.577 11.011  1.00 47.30      B1
ATOM  1723  CD2 LEU  250     11.286  26.772 12.441  1.00 46.18      B1
ATOM  1724  C   LEU  250     14.852  24.207 14.626  1.00 43.96      B1
ATOM  1725  O   LEU  250     14.450  23.887 15.764  1.00 44.07      B1
ATOM  1726  N   LEU  251     15.691  23.446 13.893  1.00 42.41      B1
ATOM  1727  H   LEU  251     16.049  23.788 13.048  1.00  0.00      B1
ATOM  1728  CA  LEU  251     16.155  22.159 14.362  1.00 40.64      B1
ATOM  1729  CB  LEU  251     16.834  21.418 13.257  1.00 36.57      B1
ATOM  1730  CG  LEU  251     15.996  20.629 12.267  1.00 34.36      B1
ATOM  1731  CD1 LEU  251     14.595  21.168 11.956  1.00 33.36      B1
ATOM  1732  CD2 LEU  251     16.875  20.619 11.050  1.00 34.71      B1
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FIGURE 5

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ATOM  1733  C   LEU   251      17.104  22.372  15.493  1.00 42.78      B1
ATOM  1734  O   LEU   251      17.124  21.554  16.395  1.00 45.44      B1
ATOM  1735  N   GLY   252      17.826  23.477  15.610  1.00 44.86      B1
ATOM  1736  H   GLY   252      17.750  24.160  14.910  1.00  0.00      B1
ATOM  1737  CA  GLY   252      18.734  23.711  16.719  1.00 46.68      B1
ATOM  1738  C   GLY   252      18.071  23.596  18.067  1.00 49.18      B1
ATOM  1739  O   GLY   252      18.709  23.318  19.077  1.00 49.23      B1
ATOM  1740  N   HIS   253      16.756  23.787  18.046  1.00 53.74      B1
ATOM  1741  H   HIS   253      16.358  24.055  17.190  1.00  0.00      B1
ATOM  1742  CA  HIS   253      15.859  23.649  19.197  1.00 57.46      B1
ATOM  1743  CB  HIS   253      14.468  24.157  18.764  1.00 62.93      B1
ATOM  1744  CG  HIS   253      13.212  23.813  19.577  1.00 68.75      B1
ATOM  1745  CD2 HIS   253      12.031  24.529  19.414  1.00 71.00      B1
ATOM  1746  ND1 HIS   253      12.980  22.854  20.479  1.00 70.67      B1
ATOM  1747  HD1 HIS   253      13.627  22.193  20.830  1.00  0.00      B1
ATOM  1748  CE1 HIS   253      11.723  22.966  20.845  1.00 73.40      B1
ATOM  1749  NE2 HIS   253      11.156  23.973  20.204  1.00 72.91      B1
ATOM  1750  HE2 HIS   253      10.218  24.260  20.311  1.00  0.00      B1
ATOM  1751  C   HIS   253      15.771  22.209  19.691  1.00 56.06      B1
ATOM  1752  O   HIS   253      15.880  21.827  20.857  1.00 56.17      B1
ATOM  1753  N   SER   254      15.395  21.435  18.724  1.00 53.46      B1
ATOM  1754  H   SER   254      15.278  21.783  17.813  1.00  0.00      B1
ATOM  1755  CA  SER   254      15.177  20.034  18.898  1.00 52.61      B1
ATOM  1756  CB  SER   254      14.613  19.595  17.576  1.00 53.04      B1
ATOM  1757  OG  SER   254      13.793  20.686  17.158  1.00 56.04      B1
ATOM  1758  HG  SER   254      13.369  20.467  16.319  1.00  0.00      B1
ATOM  1759  C   SER   254      16.512  19.386  19.275  1.00 51.48      B1
ATOM  1760  O   SER   254      16.596  18.639  20.245  1.00 51.90      B1
ATOM  1761  N   LEU   255      17.577  19.790  18.562  1.00 49.31      B1
ATOM  1762  H   LEU   255      17.430  20.480  17.889  1.00  0.00      B1
ATOM  1763  CA  LEU   255      18.913  19.272  18.723  1.00 46.02      B1
ATOM  1764  CB  LEU   255      19.706  19.723  17.537  1.00 44.66      B1
ATOM  1765  CG  LEU   255      19.362  18.968  16.274  1.00 44.51      B1
ATOM  1766  CD1 LEU   255      19.810  19.679  15.006  1.00 43.16      B1
ATOM  1767  CD2 LEU   255      19.969  17.604  16.456  1.00 44.67      B1
ATOM  1768  C   LEU   255      19.536  19.718  20.012  1.00 46.56      B1
ATOM  1769  O   LEU   255      20.565  19.174  20.440  1.00 46.82      B1
ATOM  1770  N   GLY   256      18.918  20.759  20.581  1.00 45.93      B1
ATOM  1771  H   GLY   256      18.210  21.225  20.101  1.00  0.00      B1
ATOM  1772  CA  GLY   256      19.277  21.273  21.890  1.00 46.68      B1
ATOM  1773  C   GLY   256      20.669  21.866  21.970  1.00 47.28      B1
ATOM  1774  O   GLY   256      21.273  21.844  23.056  1.00 49.64      B1
ATOM  1775  N   ILE   257      21.143  22.441  20.849  1.00 45.74      B1
ATOM  1776  H   ILE   257      20.497  22.589  20.128  1.00  0.00      B1
ATOM  1777  CA  ILE   257      22.481  23.017  20.726  1.00 43.64      B1
ATOM  1778  CB  ILE   257      22.684  23.363  19.257  1.00 42.54      B1
ATOM  1779  CG2 ILE   257      23.988  24.110  19.073  1.00 41.05      B1
ATOM  1780  CG1 ILE   257      22.694  22.088  18.437  1.00 40.55      B1
ATOM  1781  CD  ILE   257      22.452  22.468  16.970  1.00 39.49      B1
ATOM  1782  C   ILE   257      22.559  24.246  21.616  1.00 43.27      B1
ATOM  1783  O   ILE   257      21.706  25.110  21.450  1.00 43.22      B1
ATOM  1784  N   PRO   258      23.441  24.392  22.608  1.00 43.05      B1
ATOM  1785  CD  PRO   258      24.133  23.321  23.296  1.00 43.29      B1
ATOM  1786  CA  PRO   258      23.559  25.616  23.360  1.00 43.82      B1
ATOM  1787  CB  PRO   258      24.295  25.236  24.612  1.00 41.97      B1
ATOM  1788  CG  PRO   258      25.107  24.064  24.186  1.00 43.79      B1
ATOM  1789  C   PRO   258      24.252  26.703  22.555  1.00 46.06      B1
ATOM  1790  O   PRO   258      24.983  26.513  21.560  1.00 46.59      B1
ATOM  1791  N   TRP   259      23.996  27.887  23.106  1.00 46.75      B1
ATOM  1792  H   TRP   259      23.588  27.921  23.994  1.00  0.00      B1
ATOM  1793  CA  TRP   259      24.427  29.143  22.517  1.00 45.77      B1
ATOM  1794  CB  TRP   259      23.213  30.071  22.397  1.00 46.64      B1
ATOM  1795  CG  TRP   259      23.556  31.372  21.749  1.00 47.51      B1
ATOM  1796  CD2 TRP   259      23.860  31.525  20.430  1.00 47.83      B1
ATOM  1797  CE2 TRP   259      24.154  32.888  20.392  1.00 48.47      B1
ATOM  1798  CE3 TRP   259      23.940  30.745  19.290  1.00 47.39      B1
ATOM  1799  CD1 TRP   259      23.639  32.520  22.493  1.00 48.60      B1
ATOM  1800  NE1 TRP   259      24.013  33.421  21.628  1.00 48.27      B1
ATOM  1801  HE1 TRP   259      24.224  34.344  21.870  1.00  0.00      B1
ATOM  1802  CZ2 TRP   259      24.531  33.486  19.195  1.00 47.40      B1
ATOM  1803  CZ3 TRP   259      24.317  31.344  18.097  1.00 49.07      B1
ATOM  1804  CH2 TRP   259      24.613  32.706  18.050  1.00 49.12      B1
ATOM  1805  C   TRP   259      25.459  29.727  23.440  1.00 44.01      B1
ATOM  1806  O   TRP   259      25.340  29.664  24.671  1.00 43.25      B1
ATOM  1807  N   ALA   260      26.469  30.247  22.777  1.00 43.01      B1
ATOM  1808  H   ALA   260      26.523  30.198  21.796  1.00  0.00      B1
ATOM  1809  CA  ALA   260      27.493  30.973  23.482  1.00 43.48      B1
ATOM  1810  CB  ALA   260      28.874  30.549  22.969  1.00 43.33      B1
ATOM  1811  C   ALA   260      27.249  32.486  23.216  1.00 43.41      B1
ATOM  1812  O   ALA   260      27.315  32.946  22.054  1.00 40.55      B1
ATOM  1813  N   PRO   261      26.853  33.267  24.253  1.00 42.61      B1
ATOM  1814  CD  PRO   261      26.527  32.807  25.606  1.00 42.33      B1
ATOM  1815  CA  PRO   261      26.720  34.701  24.199  1.00 42.37      B1
ATOM  1816  CB  PRO   261      25.778  34.987  25.335  1.00 41.46      B1
ATOM  1817  CG  PRO   261      26.251  34.060  26.411  1.00 40.00      B1
ATOM  1818  C   PRO   261      28.087  35.369  24.311  1.00 42.22      B1
ATOM  1819  O   PRO   261      28.988  34.956  25.037  1.00 38.82      B1
ATOM  1820  N   LEU   262      28.234  36.403  23.486  1.00 45.20      B1
ATOM  1821  H   LEU   262      27.513  36.610  22.853  1.00  0.00      B1
ATOM  1822  CA  LEU   262      29.434  37.210  23.498  1.00 46.50      B1
ATOM  1823  CB  LEU   262      30.531  36.609  22.610  1.00 45.09      B1
ATOM  1824  CG  LEU   262      31.903  37.157  22.964  1.00 42.55      B1
ATOM  1825  CD1 LEU   262      32.344  36.695  24.338  1.00 41.52      B1
ATOM  1826  CD2 LEU   262      32.850  36.730  21.900  1.00 44.21      B1
ATOM  1827  C   LEU   262      29.154  38.628  23.035  1.00 48.56      B1
ATOM  1828  O   LEU   262      29.633  39.470  23.790  1.00 48.23      B1
ATOM  1829  N   SER   263      28.388  38.956  21.960  1.00 51.33      B1
ATOM  1830  H   SER   263      27.982  38.242  21.427  1.00  0.00      B1
ATOM  1831  CA  SER   263      28.127  40.339  21.494  1.00 55.19      B1
ATOM  1832  CB  SER   263      26.871  40.511  20.612  1.00 57.17      B1
ATOM  1833  OG  SER   263      26.498  39.411  19.776  1.00 64.12      B1
ATOM  1834  HG  SER   263      26.093  38.741  20.336  1.00  0.00      B1
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FIGURE 5

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ATOM  1835  C   SER  263     27.909  41.354  22.600  1.00 56.15      B1
ATOM  1836  O   SER  263     28.744  42.243  22.753  1.00 57.88      B1
ATOM  1837  N   SER  264     26.899  41.231  23.452  1.00 56.52      B1
ATOM  1838  H   SER  264     26.277  40.478  23.415  1.00  0.00      B1
ATOM  1839  CA  SER  264     26.716  42.204  24.494  1.00 58.28      B1
ATOM  1840  CB  SER  264     25.313  41.977  25.064  1.00 58.77      B1
ATOM  1841  OG  SER  264     25.099  40.726  25.713  1.00 58.50      B1
ATOM  1842  HG  SER  264     25.385  40.832  26.632  1.00  0.00      B1
ATOM  1843  C   SER  264     27.800  42.168  25.584  1.00 59.95      B1
ATOM  1844  O   SER  264     27.610  42.805  26.620  1.00 60.44      B1
ATOM  1845  N   CYS  265     28.948  41.484  25.466  1.00 61.37      B1
ATOM  1846  H   CYS  265     29.192  41.114  24.596  1.00  0.00      B1
ATOM  1847  CA  CYS  265     29.958  41.502  26.509  1.00 62.57      B1
ATOM  1848  CB  CYS  265     30.991  40.418  26.285  1.00 64.32      B1
ATOM  1849  SG  CYS  265     32.322  40.638  27.504  1.00 71.40      B1
ATOM  1850  C   CYS  265     30.667  42.860  26.515  1.00 63.12      B1
ATOM  1851  OT1 CYS  265     31.065  43.360  25.444  1.00 63.44      B1
ATOM  1852  OT2 CYS  265     30.809  43.408  27.610  1.00 61.72      B1
ATOM  1853  CB  ALA  272     40.020  43.327  30.788  1.00 77.44      B2
ATOM  1854  C   ALA  272     38.698  41.201  30.601  1.00 76.53      B2
ATOM  1855  O   ALA  272     37.525  40.873  30.361  1.00 76.81      B2
ATOM  1856  HT1 ALA  272     37.486  43.550  30.261  1.00  0.00      B2
ATOM  1857  HT2 ALA  272     37.357  42.450  28.996  1.00  0.00      B2
ATOM  1858  N   ALA  272     37.973  43.169  29.427  1.00 76.81      B2
ATOM  1859  HT3 ALA  272     38.195  43.924  28.752  1.00  0.00      B2
ATOM  1860  CA  ALA  272     39.176  42.460  29.853  1.00 77.02      B2
ATOM  1861  N   ALA  273     39.485  40.547  31.487  1.00 74.93      B2
ATOM  1862  H   ALA  273     40.334  40.963  31.745  1.00  0.00      B2
ATOM  1863  CA  ALA  273     39.244  39.241  32.119  1.00 72.64      B2
ATOM  1864  CB  ALA  273     39.704  39.279  33.558  1.00 71.92      B2
ATOM  1865  C   ALA  273     37.872  38.599  32.118  1.00 71.60      B2
ATOM  1866  O   ALA  273     37.806  37.458  31.702  1.00 71.68      B2
ATOM  1867  N   GLY  274     36.775  39.282  32.484  1.00 70.20      B2
ATOM  1868  H   GLY  274     36.903  40.167  32.874  1.00  0.00      B2
ATOM  1869  CA  GLY  274     35.412  38.758  32.425  1.00 66.78      B2
ATOM  1870  C   GLY  274     35.050  38.437  30.990  1.00 65.05      B2
ATOM  1871  O   GLY  274     34.627  37.320  30.709  1.00 66.44      B2
ATOM  1872  N   CYS  275     35.301  39.364  30.048  1.00 62.77      B2
ATOM  1873  H   CYS  275     35.634  40.223  30.357  1.00  0.00      B2
ATOM  1874  CA  CYS  275     35.026  39.188  28.611  1.00 59.30      B2
ATOM  1875  C   CYS  275     35.875  38.063  28.054  1.00 55.89      B2
ATOM  1876  O   CYS  275     35.425  37.152  27.351  1.00 54.41      B2
ATOM  1877  CB  CYS  275     35.349  40.466  27.827  1.00 61.50      B2
ATOM  1878  SG  CYS  275     34.119  40.937  26.577  1.00 66.63      B2
ATOM  1879  N   LEU  276     37.124  38.114  28.506  1.00 52.23      B2
ATOM  1880  H   LEU  276     37.350  38.722  29.233  1.00  0.00      B2
ATOM  1881  CA  LEU  276     38.091  37.163  28.066  1.00 48.93      B2
ATOM  1882  CB  LEU  276     39.483  37.564  28.542  1.00 45.96      B2
ATOM  1883  CG  LEU  276     40.241  38.557  27.670  1.00 43.20      B2
ATOM  1884  CD1 LEU  276     41.599  38.782  28.279  1.00 44.63      B2
ATOM  1885  CD2 LEU  276     40.429  38.033  26.271  1.00 40.55      B2
ATOM  1886  C   LEU  276     37.673  35.833  28.638  1.00 47.84      B2
ATOM  1887  O   LEU  276     37.784  34.803  27.964  1.00 48.51      B2
ATOM  1888  N   ALA  277     37.074  35.840  29.804  1.00 45.56      B2
ATOM  1889  H   ALA  277     36.898  36.662  30.289  1.00  0.00      B2
ATOM  1890  CA  ALA  277     36.613  34.605  30.365  1.00 45.77      B2
ATOM  1891  CB  ALA  277     36.147  34.810  31.783  1.00 47.87      B2
ATOM  1892  C   ALA  277     35.442  34.111  29.542  1.00 45.33      B2
ATOM  1893  O   ALA  277     35.342  32.926  29.271  1.00 44.20      B2
ATOM  1894  N   GLN  278     34.592  35.000  29.049  1.00 45.13      B2
ATOM  1895  H   GLN  278     34.731  35.944  29.263  1.00  0.00      B2
ATOM  1896  CA  GLN  278     33.435  34.601  28.284  1.00 45.27      B2
ATOM  1897  CB  GLN  278     32.550  35.825  28.083  1.00 48.13      B2
ATOM  1898  CG  GLN  278     31.140  35.442  28.484  1.00 56.00      B2
ATOM  1899  CD  GLN  278     30.045  36.464  28.178  1.00 61.94      B2
ATOM  1900  OE1 GLN  278     29.048  36.530  28.896  1.00 65.95      B2
ATOM  1901  NE2 GLN  278     30.080  37.291  27.132  1.00 65.55      B2
ATOM  1902  HE21 GLN  278     30.829  37.221  26.510  1.00  0.00      B2
ATOM  1903  HE22 GLN  278     29.343  37.927  27.056  1.00  0.00      B2
ATOM  1904  C   GLN  278     33.812  33.971  26.950  1.00 43.16      B2
ATOM  1905  O   GLN  278     33.173  33.050  26.462  1.00 40.58      B2
ATOM  1906  N   LEU  279     34.869  34.476  26.331  1.00 43.32      B2
ATOM  1907  H   LEU  279     35.328  35.227  26.767  1.00  0.00      B2
ATOM  1908  CA  LEU  279     35.398  33.966  25.069  1.00 42.80      B2
ATOM  1909  CB  LEU  279     36.583  34.790  24.626  1.00 41.42      B2
ATOM  1910  CG  LEU  279     36.885  35.014  23.190  1.00 40.76      B2
ATOM  1911  CD1 LEU  279     38.239  35.647  23.130  1.00 41.76      B2
ATOM  1912  CD2 LEU  279     36.943  33.753  22.411  1.00 40.01      B2
ATOM  1913  C   LEU  279     35.876  32.554  25.341  1.00 42.92      B2
ATOM  1914  O   LEU  279     35.572  31.598  24.640  1.00 42.57      B2
ATOM  1915  N   HIS  280     36.654  32.463  26.403  1.00 43.93      B2
ATOM  1916  H   HIS  280     36.837  33.282  26.917  1.00  0.00      B2
ATOM  1917  CA  HIS  280     37.215  31.223  26.850  1.00 46.12      B2
ATOM  1918  CB  HIS  280     38.029  31.506  28.101  1.00 48.74      B2
ATOM  1919  CG  HIS  280     38.914  30.320  28.394  1.00 54.16      B2
ATOM  1920  CD2 HIS  280     40.041  30.069  27.650  1.00 56.02      B2
ATOM  1921  ND1 HIS  280     38.759  29.326  29.264  1.00 56.01      B2
ATOM  1922  HD1 HIS  280     38.012  29.203  29.890  1.00  0.00      B2
ATOM  1923  CE1 HIS  280     39.744  28.483  29.058  1.00 56.64      B2
ATOM  1924  NE2 HIS  280     40.507  28.937  28.088  1.00 56.64      B2
ATOM  1925  HE2 HIS  280     41.282  28.478  27.684  1.00  0.00      B2
ATOM  1926  C   HIS  280     36.161  30.134  27.117  1.00 45.65      B2
ATOM  1927  O   HIS  280     36.362  28.977  26.711  1.00 46.23      B2
ATOM  1928  N   SER  281     35.086  30.473  27.822  1.00 43.91      B2
ATOM  1929  H   SER  281     35.009  31.367  28.219  1.00  0.00      B2
ATOM  1930  CA  SER  281     34.008  29.574  28.105  1.00 43.53      B2
ATOM  1931  CB  SER  281     33.026  30.291  29.002  1.00 44.18      B2
ATOM  1932  OG  SER  281     33.761  30.812  30.113  1.00 47.79      B2
ATOM  1933  HG  SER  281     33.288  30.648  30.931  1.00  0.00      B2
ATOM  1934  C   SER  281     33.382  29.169  26.787  1.00 43.35      B2
ATOM  1935  O   SER  281     33.334  27.973  26.496  1.00 44.83      B2
ATOM  1936  N   GLY  282     32.977  30.120  25.940  1.00 42.44      B2
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FIGURE 5

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ATOM  1937  H   GLY  282      33.043  31.058  26.221  1.00  0.00      B2
ATOM  1938  CA  GLY  282      32.363  29.869  24.632  1.00 40.65      B2
ATOM  1939  C   GLY  282      33.175  28.937  23.755  1.00 39.06      B2
ATOM  1940  O   GLY  282      32.584  28.075  23.107  1.00 40.10      B2
ATOM  1941  N   LEU  283      34.514  29.066  23.776  1.00 37.39      B2
ATOM  1942  H   LEU  283      34.880  29.807  24.304  1.00  0.00      B2
ATOM  1943  CA  LEU  283      35.465  28.213  23.037  1.00 35.06      B2
ATOM  1944  CB  LEU  283      36.902  28.718  23.089  1.00 30.20      B2
ATOM  1945  CG  LEU  283      37.167  30.001  22.302  1.00 25.73      B2
ATOM  1946  CD1 LEU  283      38.539  30.461  22.664  1.00 24.38      B2
ATOM  1947  CD2 LEU  283      37.036  29.802  20.815  1.00 21.94      B2
ATOM  1948  C   LEU  283      35.470  26.851  23.651  1.00 34.81      B2
ATOM  1949  O   LEU  283      35.314  25.859  22.947  1.00 31.09      B2
ATOM  1950  N   PHE  284      35.533  26.842  24.973  1.00 37.62      B2
ATOM  1951  H   PHE  284      35.567  27.686  25.467  1.00  0.00      B2
ATOM  1952  CA  PHE  284      35.485  25.596  25.710  1.00 42.51      B2
ATOM  1953  CB  PHE  284      35.542  25.877  27.184  1.00 49.49      B2
ATOM  1954  CG  PHE  284      36.221  24.770  27.968  1.00 58.39      B2
ATOM  1955  CD1 PHE  284      37.265  25.108  28.816  1.00 63.05      B2
ATOM  1956  CD2 PHE  284      35.810  23.453  27.861  1.00 60.84      B2
ATOM  1957  CE1 PHE  284      37.900  24.124  29.563  1.00 65.86      B2
ATOM  1958  CE2 PHE  284      36.444  22.480  28.605  1.00 64.49      B2
ATOM  1959  CZ  PHE  284      37.486  22.810  29.455  1.00 66.32      B2
ATOM  1960  C   PHE  284      34.204  24.849  25.384  1.00 41.44      B2
ATOM  1961  O   PHE  284      34.257  23.630  25.306  1.00 41.42      B2
ATOM  1962  N   LEU  285      33.100  25.563  25.101  1.00 41.24      B2
ATOM  1963  H   LEU  285      33.192  26.534  25.174  1.00  0.00      B2
ATOM  1964  CA  LEU  285      31.781  25.025  24.730  1.00 38.92      B2
ATOM  1965  CB  LEU  285      30.727  26.139  24.807  1.00 39.05      B2
ATOM  1966  CG  LEU  285      29.292  25.740  24.481  1.00 41.16      B2
ATOM  1967  CD1 LEU  285      28.711  24.981  25.662  1.00 41.12      B2
ATOM  1968  CD2 LEU  285      28.472  26.971  24.139  1.00 39.60      B2
ATOM  1969  C   LEU  285      31.780  24.441  23.329  1.00 37.34      B2
ATOM  1970  O   LEU  285      31.245  23.351  23.095  1.00 36.97      B2
ATOM  1971  N   TYR  286      32.352  25.172  22.372  1.00 35.26      B2
ATOM  1972  H   TYR  286      32.705  26.062  22.593  1.00  0.00      B2
ATOM  1973  CA  TYR  286      32.455  24.660  21.033  1.00 35.04      B2
ATOM  1974  CB  TYR  286      32.891  25.790  20.122  1.00 34.44      B2
ATOM  1975  CG  TYR  286      31.690  26.684  19.808  1.00 34.75      B2
ATOM  1976  CD1 TYR  286      31.433  27.879  20.469  1.00 35.67      B2
ATOM  1977  CE1 TYR  286      30.313  28.620  20.158  1.00 36.90      B2
ATOM  1978  CD2 TYR  286      30.823  26.255  18.839  1.00 36.19      B2
ATOM  1979  CE2 TYR  286      29.707  26.990  18.521  1.00 37.55      B2
ATOM  1980  CZ  TYR  286      29.449  28.164  19.178  1.00 37.73      B2
ATOM  1981  OH  TYR  286      28.285  28.826  18.823  1.00 38.04      B2
ATOM  1982  HH  TYR  286      28.289  29.707  19.243  1.00  0.00      B2
ATOM  1983  C   TYR  286      33.393  23.464  20.926  1.00 34.80      B2
ATOM  1984  O   TYR  286      33.071  22.537  20.180  1.00 35.35      B2
ATOM  1985  N   ALA  287      34.527  23.339  21.636  1.00 34.66      B2
ATOM  1986  H   ALA  287      34.803  24.088  22.206  1.00  0.00      B2
ATOM  1987  CA  ALA  287      35.350  22.108  21.565  1.00 34.28      B2
ATOM  1988  CB  ALA  287      36.617  22.291  22.415  1.00 33.63      B2
ATOM  1989  C   ALA  287      34.528  20.906  22.073  1.00 33.32      B2
ATOM  1990  O   ALA  287      34.535  19.827  21.478  1.00 33.07      B2
ATOM  1991  N   GLY  288      33.723  21.118  23.111  1.00 33.19      B2
ATOM  1992  H   GLY  288      33.791  21.985  23.564  1.00  0.00      B2
ATOM  1993  CA  GLY  288      32.761  20.162  23.655  1.00 35.62      B2
ATOM  1994  C   GLY  288      31.744  19.606  22.636  1.00 36.89      B2
ATOM  1995  O   GLY  288      31.624  18.379  22.444  1.00 34.97      B2
ATOM  1996  N   LEU  289      31.037  20.536  21.966  1.00 36.69      B2
ATOM  1997  H   LEU  289      31.200  21.476  22.201  1.00  0.00      B2
ATOM  1998  CA  LEU  289      30.018  20.249  20.954  1.00 35.05      B2
ATOM  1999  CB  LEU  289      29.351  21.576  20.502  1.00 36.32      B2
ATOM  2000  CG  LEU  289      28.552  22.450  21.464  1.00 35.76      B2
ATOM  2001  CD1 LEU  289      28.256  23.821  20.890  1.00 32.66      B2
ATOM  2002  CD2 LEU  289      27.246  21.780  21.697  1.00 35.35      B2
ATOM  2003  C   LEU  289      30.536  19.519  19.714  1.00 34.21      B2
ATOM  2004  O   LEU  289      29.871  18.694  19.078  1.00 33.28      B2
ATOM  2005  N   LEU  290      31.756  19.902  19.355  1.00 33.25      B2
ATOM  2006  H   LEU  290      32.183  20.634  19.850  1.00  0.00      B2
ATOM  2007  CA  LEU  290      32.448  19.345  18.230  1.00 32.44      B2
ATOM  2008  CB  LEU  290      33.729  20.159  18.000  1.00 32.62      B2
ATOM  2009  CG  LEU  290      33.560  21.509  17.315  1.00 32.05      B2
ATOM  2010  CD1 LEU  290      34.889  22.189  17.349  1.00 32.58      B2
ATOM  2011  CD2 LEU  290      33.068  21.374  15.879  1.00 31.74      B2
ATOM  2012  C   LEU  290      32.737  17.908  18.558  1.00 31.94      B2
ATOM  2013  O   LEU  290      32.432  17.020  17.772  1.00 30.50      B2
ATOM  2014  N   GLN  291      33.249  17.711  19.770  1.00 33.58      B2
ATOM  2015  H   GLN  291      33.512  18.494  20.298  1.00  0.00      B2
ATOM  2016  CA  GLN  291      33.499  16.372  20.311  1.00 36.39      B2
ATOM  2017  CB  GLN  291      33.988  16.490  21.702  1.00 36.86      B2
ATOM  2018  CG  GLN  291      34.926  15.367  21.950  1.00 39.48      B2
ATOM  2019  CD  GLN  291      35.658  15.503  23.252  1.00 40.79      B2
ATOM  2020  OE1 GLN  291      36.457  14.626  23.549  1.00 44.80      B2
ATOM  2021  NE2 GLN  291      35.494  16.535  24.072  1.00 42.59      B2
ATOM  2022 HE21 GLN  291      34.928  17.287  23.817  1.00  0.00      B2
ATOM  2023 HE22 GLN  291      35.910  16.463  24.958  1.00  0.00      B2
ATOM  2024  C   GLN  291      32.233  15.536  20.307  1.00 36.66      B2
ATOM  2025  O   GLN  291      32.220  14.478  19.707  1.00 37.46      B2
ATOM  2026  N   ALA  292      31.143  16.023  20.913  1.00 38.37      B2
ATOM  2027  H   ALA  292      31.255  16.849  21.418  1.00  0.00      B2
ATOM  2028  CA  ALA  292      29.778  15.451  20.857  1.00 39.25      B2
ATOM  2029  CB  ALA  292      28.818  16.485  21.444  1.00 40.28      B2
ATOM  2030  C   ALA  292      29.215  14.999  19.484  1.00 38.65      B2
ATOM  2031  O   ALA  292      28.411  14.067  19.356  1.00 37.58      B2
ATOM  2032  N   LEU  293      29.614  15.702  18.430  1.00 39.00      B2
ATOM  2033  H   LEU  293      30.149  16.513  18.574  1.00  0.00      B2
ATOM  2034  CA  LEU  293      29.265  15.335  17.077  1.00 39.74      B2
ATOM  2035  CB  LEU  293      29.662  16.418  16.106  1.00 37.53      B2
ATOM  2036  CG  LEU  293      28.969  17.701  16.138  1.00 34.34      B2
ATOM  2037  CD1 LEU  293      29.547  18.582  15.053  1.00 33.88      B2
ATOM  2038  CD2 LEU  293      27.503  17.462  15.918  1.00 35.69      B2
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FIGURE 5

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ATOM  2039 C   LEU  293     29.933  14.060  16.596  1.00 40.86      B2
ATOM  2040 O   LEU  293     29.686  13.669  15.449  1.00 40.58      B2
ATOM  2041 N   GLU  294     30.887  13.495  17.365  1.00 42.12      B2
ATOM  2042 H   GLU  294     31.131  13.963  18.190  1.00  0.00      B2
ATOM  2043 CA  GLU  294     31.598  12.253  17.076  1.00 42.89      B2
ATOM  2044 CB  GLU  294     30.806  10.984  17.485  1.00 48.38      B2
ATOM  2045 CG  GLU  294     30.715  10.614  18.972  1.00 56.26      B2
ATOM  2046 CD  GLU  294     29.271  10.408  19.486  1.00 63.70      B2
ATOM  2047 OE1 GLU  294     29.058  10.603  20.702  1.00 67.72      B2
ATOM  2048 OE2 GLU  294     28.363  10.074  18.692  1.00 64.81      B2
ATOM  2049 C   GLU  294     31.972  12.068  15.632  1.00 41.53      B2
ATOM  2050 O   GLU  294     31.804  11.007  15.021  1.00 40.29      B2
ATOM  2051 N   GLY  295     32.424  13.203  15.106  1.00 40.93      B2
ATOM  2052 H   GLY  295     32.357  14.033  15.621  1.00  0.00      B2
ATOM  2053 CA  GLY  295     32.998  13.236  13.783  1.00 39.95      B2
ATOM  2054 C   GLY  295     32.027  13.230  12.634  1.00 40.60      B2
ATOM  2055 O   GLY  295     32.477  13.216  11.487  1.00 40.96      B2
ATOM  2056 N   ILE  296     30.728  13.296  12.898  1.00 41.18      B2
ATOM  2057 H   ILE  296     30.446  13.210  13.825  1.00  0.00      B2
ATOM  2058 CA  ILE  296     29.687  13.306  11.888  1.00 44.02      B2
ATOM  2059 CB  ILE  296     29.683  14.580  11.009  1.00 43.49      B2
ATOM  2060 CG2 ILE  296     28.288  14.685  10.421  1.00 40.56      B2
ATOM  2061 CG1 ILE  296     30.047  15.831  11.793  1.00 45.11      B2
ATOM  2062 CD  ILE  296     30.039  17.189  11.062  1.00 46.06      B2
ATOM  2063 C   ILE  296     29.820  12.107  10.949  1.00 46.71      B2
ATOM  2064 O   ILE  296     28.918  11.279  11.060  1.00 50.61      B2
ATOM  2065 N   SER  297     30.767  11.875  10.019  1.00 47.21      B2
ATOM  2066 H   SER  297     31.526  12.491   9.936  1.00  0.00      B2
ATOM  2067 CA  SER  297     30.810  10.646   9.234  1.00 46.73      B2
ATOM  2068 CB  SER  297     30.239  10.884   7.865  1.00 45.48      B2
ATOM  2069 OG  SER  297     30.988  11.782   7.072  1.00 46.27      B2
ATOM  2070 HG  SER  297     30.321  12.200   6.503  1.00  0.00      B2
ATOM  2071 C   SER  297     32.263  10.269   9.123  1.00 48.72      B2
ATOM  2072 O   SER  297     33.120  11.122   9.391  1.00 50.55      B2
ATOM  2073 N   PRO  298     32.655   9.069   8.697  1.00 49.68      B2
ATOM  2074 CD  PRO  298     31.782   7.964   8.334  1.00 50.62      B2
ATOM  2075 CA  PRO  298     34.049   8.701   8.458  1.00 50.33      B2
ATOM  2076 CB  PRO  298     33.948   7.308   7.856  1.00 51.53      B2
ATOM  2077 CG  PRO  298     32.576   7.266   7.231  1.00 50.43      B2
ATOM  2078 C   PRO  298     34.795   9.692   7.579  1.00 50.08      B2
ATOM  2079 O   PRO  298     35.883  10.137   7.930  1.00 50.50      B2
ATOM  2080 N   GLN  299     34.173  10.086   6.469  1.00 50.48      B2
ATOM  2081 H   GLN  299     33.279   9.729   6.296  1.00  0.00      B2
ATOM  2082 CA  GLN  299     34.749  11.050   5.550  1.00 51.74      B2
ATOM  2083 CB  GLN  299     33.898  11.236   4.301  1.00 54.33      B2
ATOM  2084 CG  GLN  299     33.095  10.067   3.725  1.00 58.11      B2
ATOM  2085 CD  GLN  299     31.658  10.086   4.259  1.00 61.49      B2
ATOM  2086 OE1 GLN  299     31.160   9.083   4.776  1.00 61.00      B2
ATOM  2087 NE2 GLN  299     30.942  11.217   4.204  1.00 62.12      B2
ATOM  2088 HE21 GLN  299     31.345  12.012   3.800  1.00  0.00      B2
ATOM  2089 HE22 GLN  299     30.034  11.191   4.566  1.00  0.00      B2
ATOM  2090 C   GLN  299     34.923  12.453   6.160  1.00 51.04      B2
ATOM  2091 O   GLN  299     35.796  13.186   5.718  1.00 53.38      B2
ATOM  2092 N   LEU  300     34.118  12.918   7.120  1.00 48.15      B2
ATOM  2093 H   LEU  300     33.383  12.351   7.437  1.00  0.00      B2
ATOM  2094 CA  LEU  300     34.272  14.220   7.745  1.00 43.32      B2
ATOM  2095 CB  LEU  300     32.856  14.719   8.021  1.00 41.39      B2
ATOM  2096 CG  LEU  300     32.073  15.546   6.974  1.00 37.99      B2
ATOM  2097 CD1 LEU  300     31.872  14.824   5.688  1.00 38.34      B2
ATOM  2098 CD2 LEU  300     30.705  15.809   7.527  1.00 37.67      B2
ATOM  2099 C   LEU  300     35.142  14.220   9.019  1.00 42.84      B2
ATOM  2100 O   LEU  300     35.558  15.278   9.541  1.00 41.56      B2
ATOM  2101 N   GLY  301     35.467  13.016   9.528  1.00 40.83      B2
ATOM  2102 H   GLY  301     35.157  12.221   9.046  1.00  0.00      B2
ATOM  2103 CA  GLY  301     36.199  12.826  10.779  1.00 36.72      B2
ATOM  2104 C   GLY  301     37.500  13.607  10.887  1.00 37.69      B2
ATOM  2105 O   GLY  301     37.665  14.406  11.809  1.00 37.31      B2
ATOM  2106 N   PRO  302     38.468  13.452   9.985  1.00 37.33      B2
ATOM  2107 CD  PRO  302     38.353  12.630   8.790  1.00 37.77      B2
ATOM  2108 CA  PRO  302     39.676  14.281   9.864  1.00 37.60      B2
ATOM  2109 CB  PRO  302     40.256  13.907   8.541  1.00 36.62      B2
ATOM  2110 CG  PRO  302     39.047  13.487   7.745  1.00 37.94      B2
ATOM  2111 C   PRO  302     39.486  15.782  10.033  1.00 37.45      B2
ATOM  2112 O   PRO  302     40.132  16.398  10.901  1.00 38.33      B2
ATOM  2113 N   THR  303     38.547  16.311   9.204  1.00 37.05      B2
ATOM  2114 H   THR  303     38.085  15.727   8.567  1.00  0.00      B2
ATOM  2115 CA  THR  303     38.119  17.705   9.128  1.00 35.81      B2
ATOM  2116 CB  THR  303     36.963  17.770   8.123  1.00 37.26      B2
ATOM  2117 OG1 THR  303     37.416  17.161   6.909  1.00 39.64      B2
ATOM  2118 HG1 THR  303     37.369  17.785   6.178  1.00  0.00      B2
ATOM  2119 CG2 THR  303     36.469  19.204   7.927  1.00 38.55      B2
ATOM  2120 C   THR  303     37.687  18.223  10.505  1.00 34.93      B2
ATOM  2121 O   THR  303     38.085  19.263  11.063  1.00 35.11      B2
ATOM  2122 N   LEU  304     36.928  17.366  11.159  1.00 33.76      B2
ATOM  2123 H   LEU  304     36.672  16.500  10.762  1.00  0.00      B2
ATOM  2124 CA  LEU  304     36.436  17.746  12.418  1.00 31.01      B2
ATOM  2125 CB  LEU  304     35.345  16.803  12.708  1.00 30.31      B2
ATOM  2126 CG  LEU  304     34.234  17.567  13.320  1.00 31.32      B2
ATOM  2127 CD1 LEU  304     33.121  17.626  12.309  1.00 28.87      B2
ATOM  2128 CD2 LEU  304     33.921  16.970  14.692  1.00 34.23      B2
ATOM  2129 C   LEU  304     37.553  17.726  13.421  1.00 31.86      B2
ATOM  2130 O   LEU  304     37.615  18.623  14.259  1.00 34.21      B2
ATOM  2131 N   ASP  305     38.510  16.811  13.326  1.00 30.56      B2
ATOM  2132 H   ASP  305     38.456  16.117  12.635  1.00  0.00      B2
ATOM  2133 CA  ASP  305     39.576  16.797  14.303  1.00 30.72      B2
ATOM  2134 CB  ASP  305     40.504  15.608  14.114  1.00 36.20      B2
ATOM  2135 CG  ASP  305     39.912  14.201  14.288  1.00 40.64      B2
ATOM  2136 OD1 ASP  305     38.976  14.040  15.103  1.00 37.52      B2
ATOM  2137 OD2 ASP  305     40.426  13.304  13.581  1.00 42.39      B2
ATOM  2138 C   ASP  305     40.435  18.034  14.238  1.00 27.56      B2
ATOM  2139 O   ASP  305     40.775  18.575  15.311  1.00 24.61      B2
ATOM  2140 N   THR  306     40.781  18.417  12.979  1.00 24.77      B2
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FIGURE 5

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ATOM  2141  H   THR  306      40.469  17.875  12.230  1.00  0.00      B2
ATOM  2142  CA  THR  306      41.553  19.633  12.751  1.00 24.39      B2
ATOM  2143  CB  THR  306      41.665  19.931  11.318  1.00 24.58      B2
ATOM  2144  OG1 THR  306      42.074  18.753  10.665  1.00 25.13      B2
ATOM  2145  HG1 THR  306      41.447  18.029  10.768  1.00  0.00      B2
ATOM  2146  CG2 THR  306      42.690  21.027  11.089  1.00 25.77      B2
ATOM  2147  C   THR  306      40.893  20.844  13.419  1.00 25.24      B2
ATOM  2148  O   THR  306      41.488  21.472  14.296  1.00 27.24      B2
ATOM  2149  N   LEU  307      39.615  21.134  13.139  1.00 25.91      B2
ATOM  2150  H   LEU  307      39.125  20.547  12.520  1.00  0.00      B2
ATOM  2151  CA  LEU  307      38.900  22.228  13.764  1.00 25.53      B2
ATOM  2152  CB  LEU  307      37.571  22.170  13.142  1.00 25.09      B2
ATOM  2153  CG  LEU  307      36.530  23.097  13.588  1.00 27.93      B2
ATOM  2154  CD1 LEU  307      37.008  24.515  13.484  1.00 29.87      B2
ATOM  2155  CD2 LEU  307      35.311  22.846  12.728  1.00 28.93      B2
ATOM  2156  C   LEU  307      38.850  22.214  15.269  1.00 27.09      B2
ATOM  2157  O   LEU  307      38.854  23.253  15.925  1.00 30.03      B2
ATOM  2158  N   GLN  308      38.875  21.044  15.879  1.00 29.09      B2
ATOM  2159  H   GLN  308      38.883  20.239  15.319  1.00  0.00      B2
ATOM  2160  CA  GLN  308      38.824  20.848  17.340  1.00 29.36      B2
ATOM  2161  CB  GLN  308      38.379  19.399  17.562  1.00 29.41      B2
ATOM  2162  CG  GLN  308      37.862  19.140  18.935  1.00 32.24      B2
ATOM  2163  CD  GLN  308      37.586  17.672  19.165  1.00 34.03      B2
ATOM  2164  OE1 GLN  308      36.973  17.023  18.311  1.00 33.48      B2
ATOM  2165  NE2 GLN  308      38.053  17.127  20.299  1.00 31.67      B2
ATOM  2166 HE21 GLN  308      38.547  17.697  20.917  1.00  0.00      B2
ATOM  2167 HE22 GLN  308      37.875  16.174  20.436  1.00  0.00      B2
ATOM  2168  C   GLN  308      40.154  21.138  18.051  1.00 28.94      B2
ATOM  2169  O   GLN  308      40.196  21.796  19.101  1.00 28.44      B2
ATOM  2170  N   LEU  309      41.269  20.671  17.460  1.00 28.78      B2
ATOM  2171  H   LEU  309      41.157  20.120  16.655  1.00  0.00      B2
ATOM  2172  CA  LEU  309      42.632  20.923  17.967  1.00 28.56      B2
ATOM  2173  CB  LEU  309      43.671  20.154  17.106  1.00 26.54      B2
ATOM  2174  CG  LEU  309      43.632  18.636  17.241  1.00 24.98      B2
ATOM  2175  CD1 LEU  309      44.595  17.935  16.353  1.00 24.17      B2
ATOM  2176  CD2 LEU  309      43.992  18.310  18.621  1.00 23.45      B2
ATOM  2177  C   LEU  309      42.893  22.416  17.909  1.00 28.24      B2
ATOM  2178  O   LEU  309      43.370  22.957  18.907  1.00 30.32      B2
ATOM  2179  N   ASP  310      42.548  23.027  16.749  1.00 26.58      B2
ATOM  2180  H   ASP  310      42.296  22.437  16.007  1.00  0.00      B2
ATOM  2181  CA  ASP  310      42.495  24.477  16.495  1.00 27.90      B2
ATOM  2182  CB  ASP  310      42.025  24.659  15.076  1.00 28.41      B2
ATOM  2183  CG  ASP  310      43.162  24.556  14.096  1.00 31.84      B2
ATOM  2184  OD1 ASP  310      42.959  24.766  12.905  1.00 31.54      B2
ATOM  2185  OD2 ASP  310      44.297  24.314  14.514  1.00 37.32      B2
ATOM  2186  C   ASP  310      41.666  25.410  17.422  1.00 27.99      B2
ATOM  2187  O   ASP  310      42.219  26.429  17.876  1.00 27.23      B2
ATOM  2188  N   VAL  311      40.374  25.086  17.725  1.00 26.29      B2
ATOM  2189  H   VAL  311      39.961  24.347  17.225  1.00  0.00      B2
ATOM  2190  CA  VAL  311      39.546  25.803  18.706  1.00 24.29      B2
ATOM  2191  CB  VAL  311      38.098  25.217  18.869  1.00 21.47      B2
ATOM  2192  CG1 VAL  311      37.341  25.915  19.949  1.00 19.01      B2
ATOM  2193  CG2 VAL  311      37.261  25.488  17.667  1.00 18.56      B2
ATOM  2194  C   VAL  311      40.270  25.638  20.020  1.00 27.21      B2
ATOM  2195  O   VAL  311      40.437  26.647  20.719  1.00 29.71      B2
ATOM  2196  N   ALA  312      40.762  24.428  20.357  1.00 27.97      B2
ATOM  2197  H   ALA  312      40.585  23.674  19.756  1.00  0.00      B2
ATOM  2198  CA  ALA  312      41.515  24.157  21.583  1.00 29.24      B2
ATOM  2199  CB  ALA  312      41.855  22.688  21.532  1.00 30.53      B2
ATOM  2200  C   ALA  312      42.778  25.026  21.784  1.00 30.06      B2
ATOM  2201  O   ALA  312      43.057  25.508  22.886  1.00 30.04      B2
ATOM  2202  N   ASP  313      43.554  25.286  20.735  1.00 31.33      B2
ATOM  2203  H   ASP  313      43.433  24.730  19.935  1.00  0.00      B2
ATOM  2204  CA  ASP  313      44.610  26.275  20.743  1.00 34.22      B2
ATOM  2205  CB  ASP  313      45.279  26.512  19.447  1.00 38.87      B2
ATOM  2206  CG  ASP  313      46.071  25.404  18.866  1.00 44.55      B2
ATOM  2207  OD1 ASP  313      46.225  25.439  17.636  1.00 48.67      B2
ATOM  2208  OD2 ASP  313      46.521  24.553  19.647  1.00 49.25      B2
ATOM  2209  C   ASP  313      44.187  27.699  21.059  1.00 35.12      B2
ATOM  2210  O   ASP  313      44.807  28.390  21.894  1.00 38.60      B2
ATOM  2211  N   PHE  314      43.192  28.216  20.339  1.00 33.36      B2
ATOM  2212  H   PHE  314      42.784  27.683  19.619  1.00  0.00      B2
ATOM  2213  CA  PHE  314      42.715  29.548  20.600  1.00 31.09      B2
ATOM  2214  CB  PHE  314      41.572  29.860  19.631  1.00 32.06      B2
ATOM  2215  CG  PHE  314      41.074  31.303  19.636  1.00 33.57      B2
ATOM  2216  CD1 PHE  314      39.780  31.568  19.247  1.00 31.81      B2
ATOM  2217  CD2 PHE  314      41.907  32.354  20.021  1.00 35.65      B2
ATOM  2218  CE1 PHE  314      39.318  32.857  19.240  1.00 29.15      B2
ATOM  2219  CE2 PHE  314      41.455  33.648  20.017  1.00 32.48      B2
ATOM  2220  CZ  PHE  314      40.154  33.870  19.622  1.00 32.81      B2
ATOM  2221  C   PHE  314      42.282  29.601  22.057  1.00 29.90      B2
ATOM  2222  O   PHE  314      42.658  30.550  22.764  1.00 26.87      B2
ATOM  2223  N   ALA  315      41.686  28.532  22.584  1.00 29.29      B2
ATOM  2224  H   ALA  315      41.448  27.764  22.022  1.00  0.00      B2
ATOM  2225  CA  ALA  315      41.300  28.583  23.961  1.00 31.61      B2
ATOM  2226  CB  ALA  315      40.632  27.358  24.451  1.00 32.23      B2
ATOM  2227  C   ALA  315      42.482  28.751  24.836  1.00 34.41      B2
ATOM  2228  O   ALA  315      42.361  29.437  25.853  1.00 37.66      B2
ATOM  2229  N   THR  316      43.646  28.250  24.476  1.00 36.16      B2
ATOM  2230  H   THR  316      43.745  27.778  23.625  1.00  0.00      B2
ATOM  2231  CA  THR  316      44.780  28.388  25.374  1.00 37.99      B2
ATOM  2232  CB  THR  316      45.795  27.255  25.156  1.00 41.16      B2
ATOM  2233  OG1 THR  316      45.049  26.081  25.521  1.00 45.50      B2
ATOM  2234  HG1 THR  316      44.316  25.900  24.913  1.00  0.00      B2
ATOM  2235  CG2 THR  316      47.152  27.415  25.888  1.00 40.31      B2
ATOM  2236  C   THR  316      45.458  29.710  25.177  1.00 38.47      B2
ATOM  2237  O   THR  316      45.903  30.189  26.217  1.00 39.63      B2
ATOM  2238  N   THR  317      45.620  30.287  23.970  1.00 36.53      B2
ATOM  2239  H   THR  317      45.351  29.800  23.164  1.00  0.00      B2
ATOM  2240  CA  THR  317      46.092  31.657  23.844  1.00 37.07      B2
ATOM  2241  CB  THR  317      45.866  32.098  22.392  1.00 36.01      B2
ATOM  2242  OG1 THR  317      46.752  31.352  21.575  1.00 35.31      B2
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FIGURE 5

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ATOM  2243 HG1 THR  317      46.489  30.441  21.389  1.00  0.00      B2
ATOM  2244 CG2 THR  317      46.109  33.566  22.156  1.00 34.30      B2
ATOM  2245  C  THR  317      45.338  32.597  24.832  1.00 39.30      B2
ATOM  2246  O  THR  317      45.941  33.378  25.583  1.00 40.17      B2
ATOM  2247  N  ILE  318      44.003  32.481  24.912  1.00 40.83      B2
ATOM  2248  H  ILE  318      43.554  31.819  24.342  1.00  0.00      B2
ATOM  2249 CA  ILE  318      43.172  33.317  25.788  1.00 40.75      B2
ATOM  2250 CB  ILE  318      41.621  32.979  25.567  1.00 37.17      B2
ATOM  2251 CG2 ILE  318      40.742  33.706  26.545  1.00 34.29      B2
ATOM  2252 CG1 ILE  318      41.216  33.310  24.160  1.00 31.39      B2
ATOM  2253 CD  ILE  318      41.626  34.657  23.614  1.00 29.66      B2
ATOM  2254  C  ILE  318      43.624  33.019  27.217  1.00 42.43      B2
ATOM  2255  O  ILE  318      44.064  33.963  27.856  1.00 42.54      B2
ATOM  2256  N  TRP  319      43.662  31.784  27.744  1.00 44.17      B2
ATOM  2257  H  TRP  319      43.537  31.008  27.163  1.00  0.00      B2
ATOM  2258 CA  TRP  319      43.994  31.633  29.142  1.00 46.90      B2
ATOM  2259 CB  TRP  319      43.892  30.179  29.597  1.00 50.64      B2
ATOM  2260 CG  TRP  319      43.998  30.094  31.131  1.00 56.05      B2
ATOM  2261 CD2 TRP  319      43.005  30.397  32.038  1.00 58.61      B2
ATOM  2262 CE2 TRP  319      43.685  30.281  33.251  1.00 60.50      B2
ATOM  2263 CE3 TRP  319      41.668  30.740  32.005  1.00 60.12      B2
ATOM  2264 CD1 TRP  319      45.188  29.788  31.760  1.00 58.07      B2
ATOM  2265 NE1 TRP  319      44.968  29.921  33.042  1.00 60.07      B2
ATOM  2266 HE1 TRP  319      45.637  29.765  33.740  1.00  0.00      B2
ATOM  2267 CZ2 TRP  319      43.044  30.512  34.456  1.00 61.00      B2
ATOM  2268 CZ3 TRP  319      41.022  30.967  33.210  1.00 61.58      B2
ATOM  2269 CH2 TRP  319      41.704  30.854  34.417  1.00 62.04      B2
ATOM  2270  C  TRP  319      45.398  32.136  29.456  1.00 47.85      B2
ATOM  2271  O  TRP  319      45.635  32.772  30.490  1.00 47.99      B2
ATOM  2272  N  GLN  320      46.339  31.915  28.550  1.00 48.63      B2
ATOM  2273  H  GLN  320      46.091  31.482  27.708  1.00  0.00      B2
ATOM  2274 CA  GLN  320      47.706  32.319  28.767  1.00 49.45      B2
ATOM  2275 CB  GLN  320      48.567  31.988  27.589  1.00 51.44      B2
ATOM  2276 CG  GLN  320      48.828  30.494  27.444  1.00 55.03      B2
ATOM  2277 CD  GLN  320      49.958  30.349  26.438  1.00 60.17      B2
ATOM  2278 OE1 GLN  320      51.116  30.465  26.834  1.00 65.26      B2
ATOM  2279 NE2 GLN  320      49.771  30.145  25.131  1.00 59.32      B2
ATOM  2280 HE21 GLN  320      48.859  30.087  24.789  1.00  0.00      B2
ATOM  2281 HE22 GLN  320      50.582  30.083  24.590  1.00  0.00      B2
ATOM  2282  C  GLN  320      47.717  33.790  28.983  1.00 49.62      B2
ATOM  2283  O  GLN  320      48.251  34.209  29.987  1.00 49.91      B2
ATOM  2284  N  GLN  321      46.998  34.538  28.150  1.00 51.76      B2
ATOM  2285  H  GLN  321      46.535  34.102  27.403  1.00  0.00      B2
ATOM  2286 CA  GLN  321      46.837  35.988  28.278  1.00 52.08      B2
ATOM  2287 CB  GLN  321      46.015  36.571  27.151  1.00 49.72      B2
ATOM  2288 CG  GLN  321      45.873  38.058  27.166  1.00 51.19      B2
ATOM  2289 CD  GLN  321      47.211  38.781  27.201  1.00 53.13      B2
ATOM  2290 OE1 GLN  321      48.090  38.622  26.364  1.00 55.36      B2
ATOM  2291 NE2 GLN  321      47.468  39.618  28.177  1.00 53.21      B2
ATOM  2292 HE21 GLN  321      46.800  39.713  28.889  1.00  0.00      B2
ATOM  2293 HE22 GLN  321      48.338  40.057  28.168  1.00  0.00      B2
ATOM  2294  C  GLN  321      46.112  36.315  29.562  1.00 53.30      B2
ATOM  2295  O  GLN  321      46.293  37.422  30.058  1.00 54.39      B2
ATOM  2296  N  MET  322      45.269  35.441  30.117  1.00 54.50      B2
ATOM  2297  H  MET  322      45.098  34.592  29.662  1.00  0.00      B2
ATOM  2298 CA  MET  322      44.619  35.748  31.375  1.00 55.42      B2
ATOM  2299 CB  MET  322      43.595  34.690  31.713  1.00 52.93      B2
ATOM  2300 CG  MET  322      42.527  34.865  30.658  1.00 51.76      B2
ATOM  2301 SD  MET  322      40.861  34.428  31.189  1.00 54.19      B2
ATOM  2302 CE  MET  322      40.293  33.192  30.069  1.00 52.53      B2
ATOM  2303  C  MET  322      45.700  35.811  32.432  1.00 57.69      B2
ATOM  2304  O  MET  322      45.781  36.739  33.248  1.00 57.85      B2
ATOM  2305  N  GLU  323      46.652  34.900  32.319  1.00 60.28      B2
ATOM  2306  H  GLU  323      46.637  34.296  31.544  1.00  0.00      B2
ATOM  2307 CA  GLU  323      47.741  34.875  33.273  1.00 62.99      B2
ATOM  2308 CB  GLU  323      48.558  33.635  32.957  1.00 65.81      B2
ATOM  2309 CG  GLU  323      47.640  32.423  32.918  1.00 68.36      B2
ATOM  2310 CD  GLU  323      48.303  31.125  33.310  1.00 71.21      B2
ATOM  2311 OE1 GLU  323      47.651  30.364  34.044  1.00 71.19      B2
ATOM  2312 OE2 GLU  323      49.451  30.900  32.884  1.00 72.43      B2
ATOM  2313  C  GLU  323      48.648  36.124  33.418  1.00 63.96      B2
ATOM  2314 OT1 GLU  323      48.782  36.492  34.584  1.00 64.11      B2
ATOM  2315 OT2 GLU  323      49.169  36.725  32.449  1.00 62.96      B2
ATOM  2316 CB  MET  338      27.559  17.690  25.056  1.00 62.56      B3
ATOM  2317 CG  MET  338      28.087  18.862  24.222  1.00 63.85      B3
ATOM  2318 SD  MET  338      28.738  20.224  25.219  1.00 66.95      B3
ATOM  2319 CE  MET  338      27.328  21.252  25.515  1.00 65.50      B3
ATOM  2320  C  MET  338      24.988  17.301  25.122  1.00 57.55      B3
ATOM  2321  O  MET  338      24.417  16.347  25.667  1.00 56.47      B3
ATOM  2322 HT1 MET  338      26.255  16.010  26.594  1.00  0.00      B3
ATOM  2323 HT2 MET  338      25.375  17.061  27.500  1.00  0.00      B3
ATOM  2324  N  MET  338      26.286  16.971  27.009  1.00 61.55      B3
ATOM  2325 HT3 MET  338      27.108  17.107  27.620  1.00  0.00      B3
ATOM  2326 CA  MET  338      26.226  17.853  25.851  1.00 60.35      B3
ATOM  2327  N  PRO  339      24.493  17.830  23.998  1.00 55.58      B3
ATOM  2328 CD  PRO  339      24.914  19.075  23.375  1.00 54.39      B3
ATOM  2329 CA  PRO  339      23.453  17.226  23.164  1.00 54.62      B3
ATOM  2330 CB  PRO  339      23.463  18.098  21.903  1.00 53.52      B3
ATOM  2331 CG  PRO  339      24.845  18.711  21.909  1.00 53.04      B3
ATOM  2332  C  PRO  339      23.666  15.748  22.881  1.00 53.61      B3
ATOM  2333  O  PRO  339      24.730  15.222  23.169  1.00 53.35      B3
ATOM  2334  N  ALA  340      22.704  15.045  22.333  1.00 54.32      B3
ATOM  2335  H  ALA  340      21.844  15.460  22.111  1.00  0.00      B3
ATOM  2336 CA  ALA  340      22.909  13.651  21.968  1.00 56.04      B3
ATOM  2337 CB  ALA  340      21.867  12.713  22.625  1.00 57.60      B3
ATOM  2338  C  ALA  340      22.617  13.713  20.495  1.00 55.61      B3
ATOM  2339  O  ALA  340      21.426  13.783  20.196  1.00 58.64      B3
ATOM  2340  N  PHE  341      23.516  13.734  19.514  1.00 53.34      B3
ATOM  2341  H  PHE  341      24.472  13.607  19.685  1.00  0.00      B3
ATOM  2342 CA  PHE  341      23.016  13.900  18.158  1.00 49.92      B3
ATOM  2343 CB  PHE  341      24.050  14.541  17.244  1.00 48.16      B3
ATOM  2344 CG  PHE  341      24.382  15.940  17.658  1.00 45.00      B3
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FIGURE 5

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ATOM  2345 CD1 PHE  341      23.510  16.923  17.359  1.00 43.44      B3
ATOM  2346 CD2 PHE  341      25.527  16.175  18.388  1.00 47.03      B3
ATOM  2347 CE1 PHE  341      23.812  18.172  17.831  1.00 49.15      B3
ATOM  2348 CE2 PHE  341      25.827  17.426  18.862  1.00 47.86      B3
ATOM  2349 CZ  PHE  341      24.952  18.437  18.580  1.00 48.36      B3
ATOM  2350 C   PHE  341      22.684  12.510  17.672  1.00 49.56      B3
ATOM  2351 O   PHE  341      23.309  11.938  16.781  1.00 51.46      B3
ATOM  2352 N   ALA  342      21.625  11.985  18.245  1.00 47.40      B3
ATOM  2353 H   ALA  342      21.026  12.585  18.741  1.00  0.00      B3
ATOM  2354 CA  ALA  342      21.167  10.650  17.997  1.00 46.11      B3
ATOM  2355 CB  ALA  342      19.874  10.531  18.804  1.00 47.10      B3
ATOM  2356 C   ALA  342      20.962  10.149  16.556  1.00 44.37      B3
ATOM  2357 O   ALA  342      20.138   9.247  16.418  1.00 45.65      B3
ATOM  2358 N   SER  343      21.537  10.573  15.423  1.00 41.37      B3
ATOM  2359 H   SER  343      22.191  11.301  15.428  1.00  0.00      B3
ATOM  2360 CA  SER  343      21.274   9.923  14.145  1.00 38.80      B3
ATOM  2361 CB  SER  343      19.842  10.138  13.656  1.00 38.79      B3
ATOM  2362 OG  SER  343      19.205  11.300  14.182  1.00 37.75      B3
ATOM  2363 HG  SER  343      18.963  11.059  15.092  1.00  0.00      B3
ATOM  2364 C   SER  343      22.172  10.467  13.088  1.00 38.22      B3
ATOM  2365 O   SER  343      22.810  11.471  13.382  1.00 38.30      B3
ATOM  2366 N   ALA  344      22.206   9.845  11.888  1.00 36.73      B3
ATOM  2367 H   ALA  344      21.762   8.978  11.805  1.00  0.00      B3
ATOM  2368 CA  ALA  344      22.914  10.384  10.715  1.00 38.09      B3
ATOM  2369 CB  ALA  344      22.583   9.640   9.422  1.00 36.78      B3
ATOM  2370 C   ALA  344      22.472  11.842  10.496  1.00 37.72      B3
ATOM  2371 O   ALA  344      23.271  12.765  10.676  1.00 38.42      B3
ATOM  2372 N   PHE  345      21.194  12.042  10.163  1.00 36.10      B3
ATOM  2373 H   PHE  345      20.668  11.298   9.811  1.00  0.00      B3
ATOM  2374 CA  PHE  345      20.564  13.338  10.195  1.00 34.69      B3
ATOM  2375 CB  PHE  345      19.040  13.254  10.128  1.00 33.24      B3
ATOM  2376 CG  PHE  345      18.462  14.656   9.918  1.00 31.72      B3
ATOM  2377 CD1 PHE  345      17.715  15.223  10.905  1.00 26.64      B3
ATOM  2378 CD2 PHE  345      18.767  15.343   8.745  1.00 29.99      B3
ATOM  2379 CE1 PHE  345      17.284  16.503  10.682  1.00 33.56      B3
ATOM  2380 CE2 PHE  345      18.333  16.619   8.537  1.00 30.81      B3
ATOM  2381 CZ  PHE  345      17.581  17.281   9.520  1.00 31.44      B3
ATOM  2382 C   PHE  345      20.888  14.145  11.458  1.00 35.02      B3
ATOM  2383 O   PHE  345      21.246  15.319  11.292  1.00 37.81      B3
ATOM  2384 N   GLN  346      20.814  13.688  12.691  1.00 32.53      B3
ATOM  2385 H   GLN  346      20.516  12.778  12.894  1.00  0.00      B3
ATOM  2386 CA  GLN  346      21.156  14.586  13.758  1.00 33.46      B3
ATOM  2387 CB  GLN  346      20.899  13.985  15.061  1.00 33.80      B3
ATOM  2388 CG  GLN  346      19.459  14.284  15.174  1.00 35.68      B3
ATOM  2389 CD  GLN  346      18.788  13.658  16.344  1.00 38.48      B3
ATOM  2390 OE1 GLN  346      19.358  13.328  17.374  1.00 41.78      B3
ATOM  2391 NE2 GLN  346      17.508  13.463  16.167  1.00 41.08      B3
ATOM  2392 HE21 GLN  346      17.088  13.724  15.323  1.00  0.00      B3
ATOM  2393 HE22 GLN  346      17.026  13.063  16.919  1.00  0.00      B3
ATOM  2394 C   GLN  346      22.564  15.051  13.773  1.00 35.73      B3
ATOM  2395 O   GLN  346      22.766  16.231  14.051  1.00 38.18      B3
ATOM  2396 N   ARG  347      23.507  14.190  13.431  1.00 35.57      B3
ATOM  2397 H   ARG  347      23.248  13.289  13.157  1.00  0.00      B3
ATOM  2398 CA  ARG  347      24.907  14.538  13.396  1.00 35.95      B3
ATOM  2399 CB  ARG  347      25.760  13.236  13.222  1.00 36.29      B3
ATOM  2400 CG  ARG  347      26.198  12.549  14.540  1.00 37.41      B3
ATOM  2401 CD  ARG  347      26.986  11.246  14.373  1.00 39.70      B3
ATOM  2402 NE  ARG  347      26.072  10.167  14.028  1.00 47.18      B3
ATOM  2403 HE  ARG  347      25.416   9.893  14.701  1.00  0.00      B3
ATOM  2404 CZ  ARG  347      26.071   9.516  12.846  1.00 48.49      B3
ATOM  2405 NH1 ARG  347      26.938   9.802  11.882  1.00 50.22      B3
ATOM  2406 HH11 ARG  347      27.602  10.528  12.031  1.00  0.00      B3
ATOM  2407 HH12 ARG  347      26.905   9.313  11.011  1.00  0.00      B3
ATOM  2408 NH2 ARG  347      25.130   8.608  12.574  1.00 48.46      B3
ATOM  2409 HH21 ARG  347      24.423   8.408  13.252  1.00  0.00      B3
ATOM  2410 HH22 ARG  347      25.126   8.131  11.697  1.00  0.00      B3
ATOM  2411 C   ARG  347      25.183  15.544  12.267  1.00 35.54      B3
ATOM  2412 O   ARG  347      25.877  16.549  12.445  1.00 36.73      B3
ATOM  2413 N   ARG  348      24.611  15.353  11.096  1.00 34.74      B3
ATOM  2414 H   ARG  348      24.043  14.559  11.005  1.00  0.00      B3
ATOM  2415 CA  ARG  348      24.802  16.225   9.954  1.00 35.24      B3
ATOM  2416 CB  ARG  348      24.091  15.623   8.751  1.00 36.76      B3
ATOM  2417 CG  ARG  348      24.778  14.303   8.450  1.00 44.22      B3
ATOM  2418 CD  ARG  348      24.014  13.379   7.529  1.00 49.23      B3
ATOM  2419 NE  ARG  348      24.705  12.090   7.457  1.00 54.27      B3
ATOM  2420 HE  ARG  348      25.300  11.836   8.193  1.00  0.00      B3
ATOM  2421 CZ  ARG  348      24.557  11.226   6.430  1.00 53.75      B3
ATOM  2422 NH1 ARG  348      23.758  11.479   5.381  1.00 51.85      B3
ATOM  2423 HH11 ARG  348      23.234  12.329   5.339  1.00  0.00      B3
ATOM  2424 HH12 ARG  348      23.680  10.807   4.645  1.00  0.00      B3
ATOM  2425 NH2 ARG  348      25.252  10.083   6.462  1.00 54.51      B3
ATOM  2426 HH21 ARG  348      25.169   9.424   5.714  1.00  0.00      B3
ATOM  2427 HH22 ARG  348      25.860   9.894   7.232  1.00  0.00      B3
ATOM  2428 C   ARG  348      24.283  17.629  10.237  1.00 34.80      B3
ATOM  2429 O   ARG  348      25.078  18.564  10.219  1.00 35.16      B3
ATOM  2430 N   ALA  349      23.008  17.795  10.607  1.00 33.85      B3
ATOM  2431 H   ALA  349      22.470  16.984  10.755  1.00  0.00      B3
ATOM  2432 CA  ALA  349      22.352  19.083  10.853  1.00 32.96      B3
ATOM  2433 CB  ALA  349      20.809  18.894  11.070  1.00 33.36      B3
ATOM  2434 C   ALA  349      22.945  19.746  12.083  1.00 31.84      B3
ATOM  2435 O   ALA  349      22.981  20.969  12.210  1.00 30.69      B3
ATOM  2436 N   GLY  350      23.444  18.954  13.018  1.00 31.30      B3
ATOM  2437 H   GLY  350      23.308  17.984  12.976  1.00  0.00      B3
ATOM  2438 CA  GLY  350      24.117  19.505  14.181  1.00 31.08      B3
ATOM  2439 C   GLY  350      25.462  20.025  13.753  1.00 30.79      B3
ATOM  2440 O   GLY  350      25.974  21.010  14.280  1.00 31.38      B3
ATOM  2441 N   GLY  351      25.991  19.374  12.731  1.00 30.03      B3
ATOM  2442 H   GLY  351      25.546  18.582  12.367  1.00  0.00      B3
ATOM  2443 CA  GLY  351      27.263  19.735  12.184  1.00 29.95      B3
ATOM  2444 C   GLY  351      27.182  21.097  11.534  1.00 29.25      B3
ATOM  2445 O   GLY  351      27.937  21.974  11.919  1.00 28.74      B3
ATOM  2446 N   VAL  352      26.336  21.285  10.522  1.00 28.92      B3
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FIGURE 5

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ATOM  2447  H   VAL  352     25.859  20.484  10.214  1.00  0.00      B3
ATOM  2448  CA  VAL  352     26.079  22.567   9.881  1.00 28.59      B3
ATOM  2449  CB  VAL  352     24.845  22.452   9.004  1.00 28.96      B3
ATOM  2450  CG1 VAL  352     24.627  23.785   8.346  1.00 30.86      B3
ATOM  2451  CG2 VAL  352     25.021  21.475   7.875  1.00 26.94      B3
ATOM  2452  C   VAL  352     25.849  23.709  10.890  1.00 29.29      B3
ATOM  2453  O   VAL  352     26.520  24.747  10.853  1.00 31.02      B3
ATOM  2454  N   LEU  353     24.923  23.543  11.819  1.00 27.52      B3
ATOM  2455  H   LEU  353     24.404  22.709  11.838  1.00  0.00      B3
ATOM  2456  CA  LEU  353     24.635  24.548  12.817  1.00 26.18      B3
ATOM  2457  CB  LEU  353     23.434  24.113  13.636  1.00 27.87      B3
ATOM  2458  CG  LEU  353     22.098  24.034  12.931  1.00 26.54      B3
ATOM  2459  CD1 LEU  353     21.064  23.617  13.924  1.00 25.49      B3
ATOM  2460  CD2 LEU  353     21.750  25.372  12.320  1.00 28.23      B3
ATOM  2461  C   LEU  353     25.742  24.905  13.772  1.00 27.17      B3
ATOM  2462  O   LEU  353     25.838  26.093  14.088  1.00 28.00      B3
ATOM  2463  N   VAL  354     26.539  23.949  14.318  1.00 27.20      B3
ATOM  2464  H   VAL  354     26.321  23.006  14.139  1.00  0.00      B3
ATOM  2465  CA  VAL  354     27.712  24.212  15.157  1.00 24.62      B3
ATOM  2466  CB  VAL  354     28.236  22.910  15.745  1.00 22.01      B3
ATOM  2467  CG1 VAL  354     29.568  23.089  16.406  1.00 19.82      B3
ATOM  2468  CG2 VAL  354     27.276  22.467  16.802  1.00 23.96      B3
ATOM  2469  C   VAL  354     28.812  24.893  14.332  1.00 25.46      B3
ATOM  2470  O   VAL  354     29.439  25.832  14.798  1.00 26.23      B3
ATOM  2471  N   ALA  355     29.059  24.530  13.089  1.00 26.12      B3
ATOM  2472  H   ALA  355     28.579  23.745  12.744  1.00  0.00      B3
ATOM  2473  CA  ALA  355     30.025  25.180  12.235  1.00 26.54      B3
ATOM  2474  CB  ALA  355     30.034  24.591  10.869  1.00 22.08      B3
ATOM  2475  C   ALA  355     29.533  26.601  12.096  1.00 28.51      B3
ATOM  2476  O   ALA  355     30.315  27.498  12.344  1.00 31.93      B3
ATOM  2477  N   SER  356     28.271  26.884  11.802  1.00 30.30      B3
ATOM  2478  H   SER  356     27.654  26.134  11.665  1.00  0.00      B3
ATOM  2479  CA  SER  356     27.778  28.249  11.625  1.00 31.10      B3
ATOM  2480  CB  SER  356     26.401  28.147  11.016  1.00 35.23      B3
ATOM  2481  OG  SER  356     25.679  29.380  10.905  1.00 43.82      B3
ATOM  2482  HG  SER  356     26.250  30.004  10.429  1.00  0.00      B3
ATOM  2483  C   SER  356     27.763  29.096  12.901  1.00 29.75      B3
ATOM  2484  O   SER  356     28.115  30.289  12.898  1.00 28.35      B3
ATOM  2485  N   HIS  357     27.465  28.464  14.025  1.00 27.82      B3
ATOM  2486  H   HIS  357     27.301  27.498  14.019  1.00  0.00      B3
ATOM  2487  CA  HIS  357     27.434  29.194  15.259  1.00 26.58      B3
ATOM  2488  CB  HIS  357     26.735  28.365  16.305  1.00 25.77      B3
ATOM  2489  CG  HIS  357     25.219  28.360  16.063  1.00 27.67      B3
ATOM  2490  CD2 HIS  357     24.563  28.767  14.915  1.00 28.94      B3
ATOM  2491  ND1 HIS  357     24.277  27.963  16.915  1.00 28.43      B3
ATOM  2492  HD1 HIS  357     24.456  27.622  17.828  1.00  0.00      B3
ATOM  2493  CE1 HIS  357     23.112  28.103  16.337  1.00 28.64      B3
ATOM  2494  NE2 HIS  357     23.298  28.589  15.130  1.00 29.48      B3
ATOM  2495  HE2 HIS  357     22.576  28.801  14.495  1.00  0.00      B3
ATOM  2496  C   HIS  357     28.852  29.506  15.645  1.00 27.93      B3
ATOM  2497  O   HIS  357     29.119  30.606  16.115  1.00 29.15      B3
ATOM  2498  N   LEU  358     29.830  28.637  15.383  1.00 28.33      B3
ATOM  2499  H   LEU  358     29.624  27.761  14.997  1.00  0.00      B3
ATOM  2500  CA  LEU  358     31.211  28.940  15.721  1.00 26.39      B3
ATOM  2501  CB  LEU  358     32.030  27.702  15.547  1.00 21.42      B3
ATOM  2502  CG  LEU  358     33.457  27.878  15.734  1.00 20.42      B3
ATOM  2503  CD1 LEU  358     33.805  28.078  17.165  1.00 16.79      B3
ATOM  2504  CD2 LEU  358     34.075  26.714  15.072  1.00 22.89      B3
ATOM  2505  C   LEU  358     31.721  30.067  14.822  1.00 26.45      B3
ATOM  2506  O   LEU  358     32.372  30.939  15.378  1.00 27.12      B3
ATOM  2507  N   GLN  359     31.460  30.130  13.518  1.00 26.41      B3
ATOM  2508  H   GLN  359     31.048  29.337  13.114  1.00  0.00      B3
ATOM  2509  CA  GLN  359     31.863  31.254  12.671  1.00 29.10      B3
ATOM  2510  CB  GLN  359     31.204  31.209  11.292  1.00 30.49      B3
ATOM  2511  CG  GLN  359     31.395  29.952  10.455  1.00 38.94      B3
ATOM  2512  CD  GLN  359     32.842  29.636  10.091  1.00 42.09      B3
ATOM  2513  OE1 GLN  359     33.774  29.979  10.821  1.00 46.15      B3
ATOM  2514  NE2 GLN  359     33.103  28.987   8.967  1.00 41.34      B3
ATOM  2515 HE21 GLN  359     32.341  28.706   8.412  1.00  0.00      B3
ATOM  2516 HE22 GLN  359     34.039  28.838   8.740  1.00  0.00      B3
ATOM  2517  C   GLN  359     31.512  32.621  13.254  1.00 29.39      B3
ATOM  2518  O   GLN  359     32.427  33.427  13.484  1.00 30.06      B3
ATOM  2519  N   SER  360     30.201  32.810  13.528  1.00 28.66      B3
ATOM  2520  H   SER  360     29.595  32.061  13.343  1.00  0.00      B3
ATOM  2521  CA  SER  360     29.570  34.003  14.071  1.00 27.35      B3
ATOM  2522  CB  SER  360     28.121  33.761  14.336  1.00 26.70      B3
ATOM  2523  OG  SER  360     27.493  33.539  13.078  1.00 29.72      B3
ATOM  2524  HG  SER  360     26.637  33.112  13.288  1.00  0.00      B3
ATOM  2525  C   SER  360     30.202  34.387  15.353  1.00 27.15      B3
ATOM  2526  O   SER  360     30.575  35.550  15.498  1.00 26.93      B3
ATOM  2527  N   PHE  361     30.383  33.403  16.246  1.00 25.38      B3
ATOM  2528  H   PHE  361     30.055  32.499  16.040  1.00  0.00      B3
ATOM  2529  CA  PHE  361     31.066  33.626  17.517  1.00 25.20      B3
ATOM  2530  CB  PHE  361     31.092  32.335  18.302  1.00 23.30      B3
ATOM  2531  CG  PHE  361     31.796  32.394  19.655  1.00 23.63      B3
ATOM  2532  CD1 PHE  361     31.127  32.854  20.777  1.00 22.44      B3
ATOM  2533  CD2 PHE  361     33.098  31.931  19.770  1.00 23.35      B3
ATOM  2534  CE1 PHE  361     31.772  32.834  22.000  1.00 22.78      B3
ATOM  2535  CE2 PHE  361     33.719  31.921  21.002  1.00 21.26      B3
ATOM  2536  CZ  PHE  361     33.058  32.368  22.114  1.00 19.54      B3
ATOM  2537  C   PHE  361     32.505  34.143  17.385  1.00 26.56      B3
ATOM  2538  O   PHE  361     32.914  34.979  18.183  1.00 26.76      B3
ATOM  2539  N   LEU  362     33.309  33.645  16.441  1.00 28.17      B3
ATOM  2540  H   LEU  362     32.962  32.921  15.874  1.00  0.00      B3
ATOM  2541  CA  LEU  362     34.679  34.089  16.222  1.00 28.89      B3
ATOM  2542  CB  LEU  362     35.452  33.125  15.338  1.00 28.18      B3
ATOM  2543  CG  LEU  362     35.603  31.656  15.781  1.00 29.61      B3
ATOM  2544  CD1 LEU  362     36.306  30.996  14.633  1.00 31.63      B3
ATOM  2545  CD2 LEU  362     36.374  31.433  17.055  1.00 26.38      B3
ATOM  2546  C   LEU  362     34.692  35.449  15.536  1.00 29.18      B3
ATOM  2547  O   LEU  362     35.649  36.202  15.748  1.00 27.43      B3
ATOM  2548  N   GLU  363     33.664  35.763  14.710  1.00 29.54      B3
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FIGURE 5

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ATOM  2549  H   GLU   363      33.009  33.066  14.495  1.00  0.00      B3
ATOM  2550  CA  GLU   363      33.496  37.090  14.145  1.00 30.30      B3
ATOM  2551  CB  GLU   363      32.357  37.147  13.228  1.00 30.90      B3
ATOM  2552  CG  GLU   363      32.763  36.735  11.849  1.00 38.69      B3
ATOM  2553  CD  GLU   363      33.642  37.662  11.013  1.00 42.62      B3
ATOM  2554  OE1 GLU   363      33.896  37.282   9.860  1.00 46.58      B3
ATOM  2555  OE2 GLU   363      34.051  38.734  11.488  1.00 46.47      B3
ATOM  2556  C   GLU   363      33.229  38.098  15.244  1.00 30.19      B3
ATOM  2557  O   GLU   363      33.837  39.167  15.239  1.00 30.26      B3
ATOM  2558  N   VAL   364      32.397  37.726  16.217  1.00 30.04      B3
ATOM  2559  H   VAL   364      31.888  36.898  16.100  1.00  0.00      B3
ATOM  2560  CA  VAL   364      32.178  38.522  17.400  1.00 31.90      B3
ATOM  2561  CB  VAL   364      31.014  38.021  18.269  1.00 31.41      B3
ATOM  2562  CG1 VAL   364      30.860  38.811  19.562  1.00 30.73      B3
ATOM  2563  CG2 VAL   364      29.750  38.200  17.497  1.00 29.96      B3
ATOM  2564  C   VAL   364      33.402  38.493  18.275  1.00 35.89      B3
ATOM  2565  O   VAL   364      33.683  39.535  18.855  1.00 37.54      B3
ATOM  2566  N   SER   365      34.173  37.421  18.477  1.00 38.25      B3
ATOM  2567  H   SER   365      33.971  36.577  18.030  1.00  0.00      B3
ATOM  2568  CA  SER   365      35.337  37.478  19.375  1.00 39.61      B3
ATOM  2569  CB  SER   365      36.041  36.113  19.555  1.00 43.00      B3
ATOM  2570  OG  SER   365      35.201  34.953  19.575  1.00 46.29      B3
ATOM  2571  HG  SER   365      34.270  35.189  19.644  1.00  0.00      B3
ATOM  2572  C   SER   365      36.398  38.418  18.840  1.00 38.21      B3
ATOM  2573  O   SER   365      37.103  38.989  19.662  1.00 36.91      B3
ATOM  2574  N   TYR   366      36.575  38.540  17.514  1.00 38.00      B3
ATOM  2575  H   TYR   366      36.079  37.945  16.910  1.00  0.00      B3
ATOM  2576  CA  TYR   366      37.568  39.463  16.969  1.00 39.85      B3
ATOM  2577  CB  TYR   366      37.776  39.330  15.436  1.00 38.53      B3
ATOM  2578  CG  TYR   366      38.662  40.447  14.879  1.00 38.21      B3
ATOM  2579  CD1 TYR   366      38.104  41.464  14.129  1.00 37.18      B3
ATOM  2580  CE1 TYR   366      38.918  42.495  13.678  1.00 41.77      B3
ATOM  2581  CD2 TYR   366      40.021  40.443  15.182  1.00 40.21      B3
ATOM  2582  CE2 TYR   366      40.849  41.466  14.739  1.00 40.76      B3
ATOM  2583  CZ  TYR   366      40.297  42.504  13.976  1.00 42.82      B3
ATOM  2584  OH  TYR   366      41.151  43.522  13.493  1.00 41.30      B3
ATOM  2585  HH  TYR   366      40.743  43.977  12.755  1.00  0.00      B3
ATOM  2586  C   TYR   366      37.133  40.893  17.241  1.00 40.55      B3
ATOM  2587  O   TYR   366      37.917  41.647  17.798  1.00 40.92      B3
ATOM  2588  N   ARG   367      35.933  41.309  16.853  1.00 41.88      B3
ATOM  2589  H   ARG   367      35.360  40.682  16.360  1.00  0.00      B3
ATOM  2590  CA  ARG   367      35.442  42.653  17.139  1.00 43.32      B3
ATOM  2591  CB  ARG   367      34.013  42.709  16.650  1.00 46.82      B3
ATOM  2592  CG  ARG   367      33.528  44.130  16.650  1.00 56.74      B3
ATOM  2593  CD  ARG   367      32.069  44.267  16.248  1.00 61.81      B3
ATOM  2594  NE  ARG   367      31.723  45.687  16.229  1.00 66.59      B3
ATOM  2595  HE  ARG   367      32.438  46.356  16.172  1.00  0.00      B3
ATOM  2596  CZ  ARG   367      30.458  46.091  16.308  1.00 69.75      B3
ATOM  2597  NH1 ARG   367      29.448  45.220  16.413  1.00 72.65      B3
ATOM  2598  HH11 ARG   367      29.631  44.236  16.410  1.00  0.00      B3
ATOM  2599  HH12 ARG   367      28.503  45.548  16.445  1.00  0.00      B3
ATOM  2600  NH2 ARG   367      30.160  47.375  16.162  1.00 71.64      B3
ATOM  2601  HH21 ARG   367      29.204  47.665  16.232  1.00  0.00      B3
ATOM  2602  HH22 ARG   367      30.888  48.043  16.013  1.00  0.00      B3
ATOM  2603  C   ARG   367      35.551  43.611  18.635  1.00 40.96      B3
ATOM  2604  O   ARG   367      35.994  44.090  19.012  1.00 41.10      B3
ATOM  2605  N   VAL   368      35.160  42.135  19.542  1.00 39.83      B3
ATOM  2606  H   VAL   368      34.726  41.316  19.217  1.00  0.00      B3
ATOM  2607  CA  VAL   368      35.331  42.292  20.968  1.00 37.33      B3
ATOM  2608  CB  VAL   368      34.748  41.043  21.664  1.00 35.75      B3
ATOM  2609  CG1 VAL   368      35.087  40.867  23.140  1.00 35.10      B3
ATOM  2610  CG2 VAL   368      33.259  41.230  21.586  1.00 33.28      B3
ATOM  2611  C   VAL   368      36.813  42.459  21.223  1.00 38.75      B3
ATOM  2612  O   VAL   368      37.144  43.498  21.772  1.00 40.11      B3
ATOM  2613  N   LEU   369      37.759  41.600  20.835  1.00 39.59      B3
ATOM  2614  H   LEU   369      37.492  40.818  20.308  1.00  0.00      B3
ATOM  2615  CA  LEU   369      39.180  41.780  21.148  1.00 40.05      B3
ATOM  2616  CB  LEU   369      39.984  40.601  20.679  1.00 37.15      B3
ATOM  2617  CG  LEU   369      39.831  39.335  21.426  1.00 37.54      B3
ATOM  2618  CD1 LEU   369      40.349  38.238  20.528  1.00 39.70      B3
ATOM  2619  CD2 LEU   369      40.563  39.394  22.747  1.00 36.86      B3
ATOM  2620  C   LEU   369      39.817  43.031  20.542  1.00 41.68      B3
ATOM  2621  O   LEU   369      40.711  43.654  21.144  1.00 41.50      B3
ATOM  2622  N   ARG   370      39.333  43.413  19.354  1.00 42.80      B3
ATOM  2623  H   ARG   370      38.619  42.884  18.957  1.00  0.00      B3
ATOM  2624  CA  ARG   370      39.819  44.577  18.663  1.00 44.96      B3
ATOM  2625  CB  ARG   370      39.184  44.569  17.316  1.00 42.06      B3
ATOM  2626  CG  ARG   370      39.424  45.719  16.371  1.00 43.93      B3
ATOM  2627  CD  ARG   370      40.894  45.910  16.169  1.00 45.37      B3
ATOM  2628  NE  ARG   370      41.219  46.681  14.976  1.00 48.00      B3
ATOM  2629  HE  ARG   370      40.524  46.667  14.312  1.00  0.00      B3
ATOM  2630  CZ  ARG   370      42.469  47.153  14.791  1.00 48.45      B3
ATOM  2631  NH1 ARG   370      43.443  46.961  15.691  1.00 49.33      B3
ATOM  2632  HH11 ARG   370      43.262  46.456  16.534  1.00  0.00      B3
ATOM  2633  HH12 ARG   370      44.357  47.326  15.520  1.00  0.00      B3
ATOM  2634  NH2 ARG   370      42.821  47.710  13.635  1.00 47.59      B3
ATOM  2635  HH21 ARG   370      42.163  47.785  12.889  1.00  0.00      B3
ATOM  2636  HH22 ARG   370      43.751  48.057  13.516  1.00  0.00      B3
ATOM  2637  C   ARG   370      39.386  45.740  19.558  1.00 49.12      B3
ATOM  2638  O   ARG   370      40.216  46.615  19.826  1.00 49.67      B3
ATOM  2639  N   HIS   371      38.162  45.728  20.123  1.00 52.30      B3
ATOM  2640  H   HIS   371      37.581  44.955  19.949  1.00  0.00      B3
ATOM  2641  CA  HIS   371      37.745  46.738  21.080  1.00 56.65      B3
ATOM  2642  CB  HIS   371      36.284  46.604  21.459  1.00 62.15      B3
ATOM  2643  CG  HIS   371      35.320  46.991  20.346  1.00 71.70      B3
ATOM  2644  CD2 HIS   371      35.596  47.877  19.313  1.00 75.03      B3
ATOM  2645  ND1 HIS   371      34.067  46.546  20.166  1.00 75.91      B3
ATOM  2646  HD1 HIS   371      33.594  45.897  20.732  1.00  0.00      B3
ATOM  2647  CE1 HIS   371      33.580  47.116  19.077  1.00 77.30      B3
ATOM  2648  NE2 HIS   371      34.507  47.914  18.573  1.00 77.52      B3
ATOM  2649  HE2 HIS   371      34.401  48.460  17.764  1.00  0.00      B3
ATOM  2650  C   HIS   371      38.533  46.669  22.387  1.00 56.97      B3
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FIGURE 5

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ATOM  2651  O   HIS   371      38.458  47.592  23.176  1.00 58.12      B3
ATOM  2652  N   LEU   372      39.271  45.632  22.715  1.00 56.98      B3
ATOM  2653  H   LEU   372      39.302  44.855  22.122  1.00  0.00      B3
ATOM  2654  CA  LEU   372      40.048  45.597  23.939  1.00 57.77      B3
ATOM  2655  CB  LEU   372      39.725  44.272  24.633  1.00 57.29      B3
ATOM  2656  CG  LEU   372      38.566  44.144  25.611  1.00 55.87      B3
ATOM  2657  CD1 LEU   372      37.358  44.892  25.123  1.00 55.77      B3
ATOM  2658  CD2 LEU   372      38.211  42.675  25.749  1.00 55.33      B3
ATOM  2659  C   LEU   372      41.554  45.755  23.647  1.00 58.81      B3
ATOM  2660  O   LEU   372      42.447  45.475  24.476  1.00 59.12      B3
ATOM  2661  N   ALA   373      41.942  46.168  22.447  1.00 59.27      B3
ATOM  2662  H   ALA   373      41.271  46.255  21.731  1.00  0.00      B3
ATOM  2663  CA  ALA   373      43.336  46.425  22.147  1.00 60.03      B3
ATOM  2664  CB  ALA   373      43.755  45.485  21.021  1.00 59.87      B3
ATOM  2665  C   ALA   373      43.616  47.895  21.762  1.00 61.22      B3
ATOM  2666  OT1 ALA   373      44.798  48.243  21.697  1.00 62.45      B3
ATOM  2667  OT2 ALA   373      42.682  48.700  21.583  1.00 61.55      B3
ATOM  2668  CB  LEU   410      23.866  49.243   1.118  1.00 53.10      C1
ATOM  2669  CG  LEU   410      23.982  47.812   0.738  1.00 51.85      C1
ATOM  2670  CD1 LEU   410      25.074  47.596  -0.330  1.00 52.64      C1
ATOM  2671  CD2 LEU   410      24.125  47.081   2.058  1.00 49.28      C1
ATOM  2672  C   LEU   410      22.381  51.214   1.635  1.00 52.99      C1
ATOM  2673  O   LEU   410      22.242  52.166   0.845  1.00 53.00      C1
ATOM  2674  HT1 LEU   410      22.721  50.836  -0.665  1.00  0.00      C1
ATOM  2675  HT2 LEU   410      21.194  50.178  -0.557  1.00  0.00      C1
ATOM  2676  N   LEU   410      22.198  49.968  -0.415  1.00 54.31      C1
ATOM  2677  HT3 LEU   410      22.529  49.174  -0.998  1.00  0.00      C1
ATOM  2678  CA  LEU   410      22.478  49.815   1.004  1.00 53.64      C1
ATOM  2679  N   PRO   411      22.450  51.433   2.965  1.00 52.95      C1
ATOM  2680  CD  PRO   411      22.466  50.407   4.022  1.00 52.54      C1
ATOM  2681  CA  PRO   411      22.666  52.766   3.548  1.00 53.25      C1
ATOM  2682  CB  PRO   411      22.688  52.541   5.068  1.00 52.85      C1
ATOM  2683  CG  PRO   411      23.163  51.108   5.203  1.00 52.83      C1
ATOM  2684  C   PRO   411      23.958  53.413   3.023  1.00 53.47      C1
ATOM  2685  O   PRO   411      25.073  52.878   3.167  1.00 54.02      C1
ATOM  2686  N   GLN   412      23.787  54.599   2.411  1.00 52.79      C1
ATOM  2687  H   GLN   412      22.863  54.900   2.294  1.00  0.00      C1
ATOM  2688  CA  GLN   412      24.873  55.413   1.871  1.00 50.44      C1
ATOM  2689  CB  GLN   412      24.387  56.762   1.413  1.00 52.47      C1
ATOM  2690  CG  GLN   412      25.364  57.408   0.437  1.00 56.51      C1
ATOM  2691  CD  GLN   412      25.228  56.954  -1.017  1.00 59.40      C1
ATOM  2692  OE1 GLN   412      25.869  57.506  -1.913  1.00 59.67      C1
ATOM  2693  NE2 GLN   412      24.336  56.022  -1.389  1.00 60.12      C1
ATOM  2694  HE21 GLN   412      23.734  55.616  -0.737  1.00  0.00      C1
ATOM  2695  HE22 GLN   412      24.396  55.748  -2.328  1.00  0.00      C1
ATOM  2696  C   GLN   412      25.930  55.646   2.916  1.00 48.22      C1
ATOM  2697  O   GLN   412      27.089  55.591   2.545  1.00 46.78      C1
ATOM  2698  N   SER   413      25.614  55.842   4.201  1.00 47.90      C1
ATOM  2699  H   SER   413      24.693  55.976   4.492  1.00  0.00      C1
ATOM  2700  CA  SER   413      26.696  55.984   5.144  1.00 48.75      C1
ATOM  2701  CB  SER   413      26.261  56.344   6.548  1.00 50.61      C1
ATOM  2702  OG  SER   413      27.378  56.872   7.301  1.00 53.05      C1
ATOM  2703  HG  SER   413      28.178  56.355   7.145  1.00  0.00      C1
ATOM  2704  C   SER   413      27.480  54.684   5.267  1.00 48.71      C1
ATOM  2705  O   SER   413      28.698  54.839   5.392  1.00 50.77      C1
ATOM  2706  N   PHE   414      26.947  53.440   5.208  1.00 46.01      C1
ATOM  2707  H   PHE   414      25.996  53.323   5.015  1.00  0.00      C1
ATOM  2708  CA  PHE   414      27.787  52.233   5.274  1.00 42.92      C1
ATOM  2709  CB  PHE   414      26.959  50.915   5.232  1.00 40.76      C1
ATOM  2710  CG  PHE   414      27.633  49.627   4.757  1.00 35.06      C1
ATOM  2711  CD1 PHE   414      27.583  49.256   3.425  1.00 34.71      C1
ATOM  2712  CD2 PHE   414      28.262  48.800   5.663  1.00 34.81      C1
ATOM  2713  CE1 PHE   414      28.156  48.056   3.014  1.00 36.16      C1
ATOM  2714  CE2 PHE   414      28.832  47.602   5.247  1.00 33.40      C1
ATOM  2715  CZ  PHE   414      28.781  47.223   3.923  1.00 34.22      C1
ATOM  2716  C   PHE   414      28.667  52.271   4.044  1.00 41.75      C1
ATOM  2717  O   PHE   414      29.831  51.902   4.110  1.00 41.47      C1
ATOM  2718  N   LEU   415      28.122  52.748   2.942  1.00 39.50      C1
ATOM  2719  H   LEU   415      27.188  53.044   2.946  1.00  0.00      C1
ATOM  2720  CA  LEU   415      28.865  52.769   1.721  1.00 39.91      C1
ATOM  2721  CB  LEU   415      27.946  53.205   0.641  1.00 41.98      C1
ATOM  2722  CG  LEU   415      27.903  52.274  -0.526  1.00 44.75      C1
ATOM  2723  CD1 LEU   415      26.430  51.951  -0.780  1.00 42.93      C1
ATOM  2724  CD2 LEU   415      28.793  52.853  -1.648  1.00 45.91      C1
ATOM  2725  C   LEU   415      30.081  53.669   1.755  1.00 40.03      C1
ATOM  2726  O   LEU   415      31.142  53.348   1.183  1.00 40.28      C1
ATOM  2727  N   LEU   416      29.901  54.779   2.487  1.00 37.46      C1
ATOM  2728  H   LEU   416      29.028  54.948   2.899  1.00  0.00      C1
ATOM  2729  CA  LEU   416      30.942  55.756   2.602  1.00 34.05      C1
ATOM  2730  CB  LEU   416      30.294  57.089   2.998  1.00 34.67      C1
ATOM  2731  CG  LEU   416      29.438  57.704   1.851  1.00 35.24      C1
ATOM  2732  CD1 LEU   416      28.770  58.948   2.358  1.00 31.67      C1
ATOM  2733  CD2 LEU   416      30.310  57.948   0.593  1.00 35.50      C1
ATOM  2734  C   LEU   416      31.952  55.258   3.586  1.00 31.97      C1
ATOM  2735  O   LEU   416      33.131  55.427   3.270  1.00 33.52      C1
ATOM  2736  N   ALA   417      31.573  54.619   4.695  1.00 29.05      C1
ATOM  2737  H   ALA   417      30.621  54.616   4.927  1.00  0.00      C1
ATOM  2738  CA  ALA   417      32.524  53.882   5.561  1.00 29.64      C1
ATOM  2739  CB  ALA   417      31.853  53.087   6.680  1.00 25.16      C1
ATOM  2740  C   ALA   417      33.319  52.827   4.777  1.00 30.68      C1
ATOM  2741  O   ALA   417      34.536  52.721   4.877  1.00 31.52      C1
ATOM  2742  N   CYS   418      32.726  52.041   3.905  1.00 32.19      C1
ATOM  2743  H   CYS   418      31.748  52.017   3.860  1.00  0.00      C1
ATOM  2744  CA  CYS   418      33.499  51.119   3.103  1.00 33.67      C1
ATOM  2745  CB  CYS   418      32.657  50.250   2.226  1.00 33.85      C1
ATOM  2746  SG  CYS   418      31.623  49.208   3.246  1.00 37.80      C1
ATOM  2747  C   CYS   418      34.446  51.818   2.170  1.00 34.80      C1
ATOM  2748  O   CYS   418      35.626  51.441   2.173  1.00 36.47      C1
ATOM  2749  N   LEU   419      34.009  52.820   1.377  1.00 35.09      C1
ATOM  2750  H   LEU   419      33.082  53.131   1.460  1.00  0.00      C1
ATOM  2751  CA  LEU   419      34.886  53.446   0.375  1.00 34.14      C1
ATOM  2752  CB  LEU   419      34.062  54.484  -0.413  1.00 37.09      C1
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FIGURE 5

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ATOM  2753 CG  LEU  419      32.866  5..853  -1.244  1.00 39.61      C1
ATOM  2754 CD1 LEU  419      31.866  54.918  -1.609  1.00 39.24      C1
ATOM  2755 CD2 LEU  419      33.349  53.207  -2.553  1.00 40.02      C1
ATOM  2756 C   LEU  419      36.102  54.041   1.047  1.00 32.33      C1
ATOM  2757 O   LEU  419      37.198  53.973   0.549  1.00 31.60      C1
ATOM  2758 N   GLU  420      35.974  54.483   2.273  1.00 31.92      C1
ATOM  2759 H   GLU  420      35.068  54.528   2.648  1.00  0.00      C1
ATOM  2760 CA  GLU  420      37.078  54.905   3.092  1.00 31.79      C1
ATOM  2761 CB  GLU  420      36.477  55.462   4.344  1.00 34.29      C1
ATOM  2762 CG  GLU  420      37.430  56.240   5.185  1.00 38.66      C1
ATOM  2763 CD  GLU  420      36.952  56.499   6.609  1.00 45.20      C1
ATOM  2764 OE1 GLU  420      37.873  56.849   7.367  1.00 45.67      C1
ATOM  2765 OE2 GLU  420      35.745  56.345   6.954  1.00 44.21      C1
ATOM  2766 C   GLU  420      38.043  53.763   3.423  1.00 31.87      C1
ATOM  2767 O   GLU  420      39.253  53.949   3.270  1.00 32.82      C1
ATOM  2768 N   GLN  421      37.553  52.624   3.954  1.00 30.46      C1
ATOM  2769 H   GLN  421      36.583  52.556   4.098  1.00  0.00      C1
ATOM  2770 CA  GLN  421      38.366  51.461   4.283  1.00 29.34      C1
ATOM  2771 CB  GLN  421      37.545  50.389   4.984  1.00 30.88      C1
ATOM  2772 CG  GLN  421      37.308  50.634   6.463  1.00 33.58      C1
ATOM  2773 CD  GLN  421      36.320  49.625   7.058  1.00 37.89      C1
ATOM  2774 OE1 GLN  421      35.357  49.236   6.398  1.00 43.18      C1
ATOM  2775 NE2 GLN  421      36.427  49.095   8.275  1.00 37.13      C1
ATOM  2776 HE21 GLN  421      35.695  48.505   8.556  1.00  0.00      C1
ATOM  2777 HE22 GLN  421      37.207  49.330   8.812  1.00  0.00      C1
ATOM  2778 C   GLN  421      38.991  50.862   3.026  1.00 27.36      C1
ATOM  2779 O   GLN  421      40.152  50.445   3.099  1.00 29.09      C1
ATOM  2780 N   VAL  422      38.379  50.845   1.847  1.00 23.57      C1
ATOM  2781 H   VAL  422      37.448  51.138   1.803  1.00  0.00      C1
ATOM  2782 CA  VAL  422      39.077  50.420   0.651  1.00 23.52      C1
ATOM  2783 CB  VAL  422      38.163  50.636  -0.556  1.00 22.67      C1
ATOM  2784 CG1 VAL  422      38.873  50.455  -1.868  1.00 21.56      C1
ATOM  2785 CG2 VAL  422      37.057  49.610  -0.465  1.00 26.79      C1
ATOM  2786 C   VAL  422      40.353  51.254   0.514  1.00 26.22      C1
ATOM  2787 O   VAL  422      41.458  50.708   0.508  1.00 28.77      C1
ATOM  2788 N   ARG  423      40.275  52.599   0.575  1.00 27.49      C1
ATOM  2789 H   ARG  423      39.402  53.016   0.735  1.00  0.00      C1
ATOM  2790 CA  ARG  423      41.436  53.456   0.346  1.00 25.91      C1
ATOM  2791 CB  ARG  423      41.098  54.943   0.312  1.00 24.39      C1
ATOM  2792 CG  ARG  423      40.167  55.366  -0.807  1.00 22.81      C1
ATOM  2793 CD  ARG  423      40.525  54.798  -2.172  1.00 25.55      C1
ATOM  2794 NE  ARG  423      39.707  55.387  -3.216  1.00 25.38      C1
ATOM  2795 HE  ARG  423      39.168  56.173  -2.989  1.00  0.00      C1
ATOM  2796 CZ  ARG  423      39.629  54.928  -4.466  1.00 27.32      C1
ATOM  2797 NH1 ARG  423      40.264  53.857  -4.949  1.00 26.37      C1
ATOM  2798 HH11 ARG  423      40.884  53.341  -4.365  1.00  0.00      C1
ATOM  2799 HH12 ARG  423      40.150  53.595  -5.907  1.00  0.00      C1
ATOM  2800 NH2 ARG  423      38.960  55.682  -5.325  1.00 30.38      C1
ATOM  2801 HH21 ARG  423      38.539  56.537  -5.023  1.00  0.00      C1
ATOM  2802 HH22 ARG  423      38.865  55.385  -6.275  1.00  0.00      C1
ATOM  2803 C   ARG  423      42.429  53.241   1.432  1.00 23.60      C1
ATOM  2804 ..  ARG  423      43.594  53.147   1.127  1.00 24.37      C1
ATOM  2805 N   LYS  424      42.065  53.050   2.668  1.00 24.38      C1
ATOM  2806 H   LYS  424      41.109  53.051   2.890  1.00  0.00      C1
ATOM  2807 CA  LYS  424      43.043  52.855   3.722  1.00 25.12      C1
ATOM  2808 CB  LYS  424      42.352  52.791   5.051  1.00 23.89      C1
ATOM  2809 CG  LYS  424      43.312  52.936   6.190  1.00 28.56      C1
ATOM  2810 CD  LYS  424      42.579  52.580   7.486  1.00 35.51      C1
ATOM  2811 CE  LYS  424      41.338  53.425   7.853  1.00 40.33      C1
ATOM  2812 NZ  LYS  424      40.519  52.722   8.834  1.00 42.23      C1
ATOM  2813 HZ1 LYS  424      41.079  52.559   9.695  1.00  0.00      C1
ATOM  2814 HZ2 LYS  424      40.208  51.814   8.435  1.00  0.00      C1
ATOM  2815 HZ3 LYS  424      39.689  53.306   9.065  1.00  0.00      C1
ATOM  2816 C   LYS  424      43.761  51.547   3.462  1.00 27.10      C1
ATOM  2817 O   LYS  424      44.923  51.425   3.848  1.00 30.64      C1
ATOM  2818 N   ILE  425      43.190  50.542   2.794  1.00 26.83      C1
ATOM  2819 H   ILE  425      42.260  50.607   2.488  1.00  0.00      C1
ATOM  2820 CA  ILE  425      43.949  49.312   2.561  1.00 25.16      C1
ATOM  2821 CB  ILE  425      42.965  48.093   2.336  1.00 24.91      C1
ATOM  2822 CG2 ILE  425      43.654  46.786   1.995  1.00 22.01      C1
ATOM  2823 CG1 ILE  425      42.229  47.909   3.633  1.00 25.34      C1
ATOM  2824 CD  ILE  425      40.885  47.169   3.432  1.00 25.68      C1
ATOM  2825 C   ILE  425      44.824  49.549   1.346  1.00 23.84      C1
ATOM  2826 O   ILE  425      45.959  49.069   1.316  1.00 24.57      C1
ATOM  2827 N   GLN  426      44.361  50.267   0.323  1.00 23.28      C1
ATOM  2828 H   GLN  426      43.451  50.630   0.393  1.00  0.00      C1
ATOM  2829 CA  GLN  426      45.164  50.531  -0.871  1.00 24.13      C1
ATOM  2830 CB  GLN  426      44.421  51.344  -1.896  1.00 24.04      C1
ATOM  2831 CG  GLN  426      43.275  50.539  -2.396  1.00 23.56      C1
ATOM  2832 CD  GLN  426      42.446  51.105  -3.511  1.00 23.92      C1
ATOM  2833 OE1 GLN  426      41.704  52.047  -3.345  1.00 25.34      C1
ATOM  2834 NE2 GLN  426      42.337  50.509  -4.672  1.00 27.55      C1
ATOM  2835 HE21 GLN  426      41.755  50.948  -5.323  1.00  0.00      C1
ATOM  2836 HE22 GLN  426      42.850  49.696  -4.851  1.00  0.00      C1
ATOM  2837 C   GLN  426      46.404  51.312  -0.488  1.00 26.69      C1
ATOM  2838 O   GLN  426      47.486  51.109  -1.046  1.00 29.73      C1
ATOM  2839 N   GLY  427      46.300  52.204   0.499  1.00 26.49      C1
ATOM  2840 H   GLY  427      45.410  52.414   0.854  1.00  0.00      C1
ATOM  2841 CA  GLY  427      47.446  52.894   1.022  1.00 24.25      C1
ATOM  2842 C   GLY  427      48.467  51.913   1.589  1.00 23.08      C1
ATOM  2843 O   GLY  427      49.597  51.921   1.106  1.00 22.28      C1
ATOM  2844 N   ASP  428      48.107  51.073   2.575  1.00 22.75      C1
ATOM  2845 H   ASP  428      47.189  51.111   2.918  1.00  0.00      C1
ATOM  2846 CA  ASP  428      49.039  50.108   3.131  1.00 23.87      C1
ATOM  2847 CB  ASP  428      48.415  49.199   4.117  1.00 26.52      C1
ATOM  2848 CG  ASP  428      47.437  49.779   5.097  1.00 28.84      C1
ATOM  2849 OD1 ASP  428      46.420  49.151   5.265  1.00 31.81      C1
ATOM  2850 OD2 ASP  428      47.662  50.804   5.716  1.00 30.77      C1
ATOM  2851 C   ASP  428      49.626  49.191   2.063  1.00 24.16      C1
ATOM  2852 O   ASP  428      50.812  48.896   2.088  1.00 26.17      C1
ATOM  2853 N   GLY  429      48.840  48.822   1.069  1.00 23.01      C1
ATOM  2854 H   GLY  429      47.905  49.113   1.071  1.00  0.00      C1
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FIGURE 5

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ATOM 2855 CA GLY 429 49.289 ..964 0.029 1.00 25.44 C1
ATOM 2856 C GLY 429 50.405 48.649 -0.716 1.00 27.39 C1
ATOM 2857 O GLY 429 51.528 48.135 -0.741 1.00 28.51 C1
ATOM 2858 N ALA 430 50.127 49.840 -1.271 1.00 28.26 C1
ATOM 2859 H ALA 430 49.216 50.185 -1.172 1.00 0.00 C1
ATOM 2860 CA ALA 430 51.094 50.643 -2.015 1.00 26.04 C1
ATOM 2861 CB ALA 430 50.490 51.976 -2.407 1.00 27.93 C1
ATOM 2862 C ALA 430 52.300 50.927 -1.133 1.00 25.19 C1
ATOM 2863 O ALA 430 53.393 51.053 -1.655 1.00 25.43 C1
ATOM 2864 N ALA 431 52.171 50.979 0.186 1.00 24.05 C1
ATOM 2865 H ALA 431 51.279 50.872 0.579 1.00 0.00 C1
ATOM 2866 CA ALA 431 53.295 51.213 1.035 1.00 26.29 C1
ATOM 2867 CB ALA 431 52.874 51.522 2.458 1.00 24.14 C1
ATOM 2868 C ALA 431 54.139 49.972 1.073 1.00 29.82 C1
ATOM 2869 O ALA 431 55.360 50.085 0.959 1.00 31.97 C1
ATOM 2870 N LEU 432 53.562 48.777 1.203 1.00 31.87 C1
ATOM 2871 H LEU 432 52.585 48.726 1.279 1.00 0.00 C1
ATOM 2872 CA LEU 432 54.337 47.540 1.165 1.00 33.92 C1
ATOM 2873 CB LEU 432 53.430 46.315 1.301 1.00 37.42 C1
ATOM 2874 CG LEU 432 54.063 44.952 1.574 1.00 37.40 C1
ATOM 2875 CD1 LEU 432 54.751 44.949 2.950 1.00 38.10 C1
ATOM 2876 CD2 LEU 432 52.966 43.901 1.492 1.00 36.27 C1
ATOM 2877 C LEU 432 55.096 47.404 -0.146 1.00 33.74 C1
ATOM 2878 O LEU 432 56.306 47.179 -0.138 1.00 33.29 C1
ATOM 2879 N GLN 433 54.402 47.564 -1.276 1.00 34.57 C1
ATOM 2880 H GLN 433 53.439 47.733 -1.186 1.00 0.00 C1
ATOM 2881 CA GLN 433 55.002 47.526 -2.600 1.00 35.83 C1
ATOM 2882 CB GLN 433 53.999 47.892 -3.664 1.00 35.52 C1
ATOM 2883 CG GLN 433 52.996 46.823 -3.832 1.00 39.40 C1
ATOM 2884 CD GLN 433 52.049 47.097 -4.973 1.00 42.46 C1
ATOM 2885 OE1 GLN 433 50.924 47.526 -4.786 1.00 48.22 C1
ATOM 2886 NE2 GLN 433 52.376 46.878 -6.225 1.00 44.77 C1
ATOM 2887 HE21 GLN 433 53.271 46.540 -6.433 1.00 0.00 C1
ATOM 2888 HE22 GLN 433 51.693 47.087 -6.892 1.00 0.00 C1
ATOM 2889 C GLN 433 56.177 48.485 -2.757 1.00 36.48 C1
ATOM 2890 O GLN 433 57.214 48.118 -3.312 1.00 38.08 C1
ATOM 2891 N GLU 434 56.055 49.719 -2.287 1.00 36.11 C1
ATOM 2892 H GLU 434 55.210 49.978 -1.854 1.00 0.00 C1
ATOM 2893 CA GLU 434 57.089 50.719 -2.426 1.00 35.93 C1
ATOM 2894 CB GLU 434 56.408 52.030 -2.068 1.00 41.28 C1
ATOM 2895 CG GLU 434 57.126 53.356 -2.019 1.00 43.07 C1
ATOM 2896 CD GLU 434 57.832 53.516 -0.698 1.00 45.70 C1
ATOM 2897 OE1 GLU 434 57.190 53.538 0.367 1.00 49.33 C1
ATOM 2898 OE2 GLU 434 59.051 53.579 -0.760 1.00 45.45 C1
ATOM 2899 C GLU 434 58.257 50.348 -1.548 1.00 34.00 C1
ATOM 2900 O GLU 434 59.388 50.481 -1.983 1.00 32.93 C1
ATOM 2901 N LYS 435 58.067 49.860 -0.330 1.00 34.34 C1
ATOM 2902 H LYS 435 57.146 49.837 0.014 1.00 0.00 C1
ATOM 2903 CA LYS 435 59.151 49.358 0.511 1.00 34.56 C1
ATOM 2904 CB LYS 435 58.577 49.010 1.847 1.00 33.89 C1
ATOM 2905 CG LYS 435 58.357 50.231 2.709 1.00 36.71 C1
ATOM 2906 CD LYS 435 58.244 49.748 4.137 1.00 40.31 C1
ATOM 2907 CE LYS 435 58.293 50.861 5.213 1.00 45.32 C1
ATOM 2908 NZ LYS 435 58.494 50.325 6.575 1.00 47.31 C1
ATOM 2909 HZ1 LYS 435 59.388 49.795 6.611 1.00 0.00 C1
ATOM 2910 HZ2 LYS 435 57.708 49.689 6.818 1.00 0.00 C1
ATOM 2911 HZ3 LYS 435 58.534 51.109 7.257 1.00 0.00 C1
ATOM 2912 C LYS 435 59.906 48.135 -0.065 1.00 36.10 C1
ATOM 2913 O LYS 435 61.139 48.036 -0.012 1.00 37.08 C1
ATOM 2914 N LEU 436 59.215 47.168 -0.665 1.00 36.28 C1
ATOM 2915 H LEU 436 58.235 47.245 -0.651 1.00 0.00 C1
ATOM 2916 CA LEU 436 59.793 45.994 -1.304 1.00 34.25 C1
ATOM 2917 CB LEU 436 58.655 45.076 -1.753 1.00 33.41 C1
ATOM 2918 CG LEU 436 57.920 44.327 -0.610 1.00 34.72 C1
ATOM 2919 CD1 LEU 436 56.764 43.538 -1.181 1.00 33.50 C1
ATOM 2920 CD2 LEU 436 58.880 43.375 0.117 1.00 36.39 C1
ATOM 2921 C LEU 436 60.669 46.383 -2.467 1.00 33.31 C1
ATOM 2922 O LEU 436 61.756 45.825 -2.647 1.00 33.94 C1
ATOM 2923 N CYS 437 60.220 47.374 -3.222 1.00 32.34 C1
ATOM 2924 H CYS 437 59.290 47.661 -3.097 1.00 0.00 C1
ATOM 2925 CA CYS 437 60.978 47.949 -4.301 1.00 32.01 C1
ATOM 2926 C CYS 437 62.214 48.704 -3.857 1.00 34.70 C1
ATOM 2927 O CYS 437 63.313 48.599 -4.412 1.00 36.26 C1
ATOM 2928 CB CYS 437 60.094 48.840 -5.008 1.00 30.97 C1
ATOM 2929 SG CYS 437 61.003 49.666 -6.319 1.00 36.22 C1
ATOM 2930 N ALA 438 62.016 49.463 -2.785 1.00 36.35 C1
ATOM 2931 H ALA 438 61.108 49.547 -2.431 1.00 0.00 C1
ATOM 2932 CA ALA 438 63.060 50.226 -2.170 1.00 35.83 C1
ATOM 2933 CB ALA 438 62.440 51.107 -1.153 1.00 36.38 C1
ATOM 2934 C ALA 438 64.065 49.294 -1.527 1.00 37.01 C1
ATOM 2935 O ALA 438 65.132 49.168 -2.092 1.00 39.39 C1
ATOM 2936 N THR 439 63.808 48.591 -0.422 1.00 36.59 C1
ATOM 2937 H THR 439 62.947 48.723 0.014 1.00 0.00 C1
ATOM 2938 CA THR 439 64.742 47.669 0.223 1.00 35.70 C1
ATOM 2939 CB THR 439 64.073 47.042 1.400 1.00 35.34 C1
ATOM 2940 OG1 THR 439 63.323 48.048 2.040 1.00 38.31 C1
ATOM 2941 HG1 THR 439 62.419 47.999 1.706 1.00 0.00 C1
ATOM 2942 CG2 THR 439 65.039 46.479 2.369 1.00 36.50 C1
ATOM 2943 C THR 439 65.331 46.517 -0.590 1.00 36.10 C1
ATOM 2944 O THR 439 66.448 46.093 -0.312 1.00 36.51 C1
ATOM 2945 N TYR 440 64.603 45.917 -1.548 1.00 36.02 C1
ATOM 2946 H TYR 440 63.751 46.319 -1.822 1.00 0.00 C1
ATOM 2947 CA TYR 440 65.057 44.691 -2.198 1.00 34.28 C1
ATOM 2948 CB TYR 440 64.175 43.480 -1.878 1.00 33.99 C1
ATOM 2949 CG TYR 440 64.016 43.240 -0.397 1.00 34.14 C1
ATOM 2950 CD1 TYR 440 62.773 43.230 0.169 1.00 35.16 C1
ATOM 2951 CE1 TYR 440 62.625 43.037 1.532 1.00 36.66 C1
ATOM 2952 CD2 TYR 440 65.126 43.064 0.385 1.00 37.84 C1
ATOM 2953 CE2 TYR 440 64.992 42.881 1.752 1.00 39.02 C1
ATOM 2954 CZ TYR 440 63.741 42.864 2.317 1.00 37.34 C1
ATOM 2955 OH TYR 440 63.637 42.649 3.678 1.00 17.56 C1
ATOM 2956 HH TYR 440 64.498 42.343 3.988 1.00 0.00 C1
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FIGURE 5

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ATOM 2957 C  TYR 440  65.088 44.768 -3.681 1.00 34.07  C1
ATOM 2958 O  TYR 440  65.598 43.823 -4.267 1.00 35.54  C1
ATOM 2959 N  LYS 441  64.627 45.833 -4.330 1.00 33.18  C1
ATOM 2960 H  LYS 441  64.345 46.623 -3.822 1.00 0.00   C1
ATOM 2961 CA LYS 441  64.595 45.957 -5.763 1.00 30.44  C1
ATOM 2962 CB LYS 441  65.983 45.759 -6.364 1.00 33.76  C1
ATOM 2963 CG LYS 441  66.729 47.080 -6.407 1.00 39.59  C1
ATOM 2964 CD LYS 441  67.273 47.497 -5.045 1.00 47.69  C1
ATOM 2965 CE LYS 441  67.503 49.028 -4.984 1.00 53.37  C1
ATOM 2966 NZ LYS 441  66.267 49.780 -5.240 1.00 57.64  C1
ATOM 2967 HZ1 LYS 441  65.568 49.549 -4.506 1.00 0.00  C1
ATOM 2968 HZ2 LYS 441  65.885 49.525 -6.173 1.00 0.00  C1
ATOM 2969 HZ3 LYS 441  66.468 50.801 -5.219 1.00 0.00  C1
ATOM 2970 C  LYS 441  63.629 45.015 -6.425 1.00 28.86  C1
ATOM 2971 O  LYS 441  63.791 44.688 -7.603 1.00 29.95  C1
ATOM 2972 N  LEU 442  62.556 44.601 -5.749 1.00 27.58  C1
ATOM 2973 H  LEU 442  62.392 44.924 -4.837 1.00 0.00   C1
ATOM 2974 CA LEU 442  61.554 43.780 -6.402 1.00 28.82  C1
ATOM 2975 CB LEU 442  60.947 42.694 -5.466 1.00 26.98  C1
ATOM 2976 CG LEU 442  61.905 41.634 -4.847 1.00 27.75  C1
ATOM 2977 CD1 LEU 442  61.133 40.643 -4.009 1.00 24.29  C1
ATOM 2978 CD2 LEU 442  62.667 40.932 -5.963 1.00 19.72  C1
ATOM 2979 C  LEU 442  60.575 44.892 -6.635 1.00 30.59  C1
ATOM 2980 O  LEU 442  59.811 45.261 -5.741 1.00 32.36  C1
ATOM 2981 N  CYS 443  60.700 45.506 -7.804 1.00 32.15  C1
ATOM 2982 H  CYS 443  61.423 45.199 -8.389 1.00 0.00   C1
ATOM 2983 CA CYS 443  59.866 46.645 -8.191 1.00 32.69  C1
ATOM 2984 C  CYS 443  58.807 46.380 -9.217 1.00 33.43  C1
ATOM 2985 O  CYS 443  58.051 47.288 -9.465 1.00 34.10  C1
ATOM 2986 CB CYS 443  60.715 47.800 -8.743 1.00 30.74  C1
ATOM 2987 SG CYS 443  61.938 48.345 -7.519 1.00 32.96  C1
ATOM 2988 N  HIS 444  58.649 45.260 -9.911 1.00 35.65  C1
ATOM 2989 H  HIS 444  59.147 44.445 -9.659 1.00 0.00   C1
ATOM 2990 CA HIS 444  57.662 45.172 -10.975 1.00 37.75  C1
ATOM 2991 CB HIS 444  58.329 45.224 -12.330 1.00 37.09  C1
ATOM 2992 CG HIS 444  59.149 46.476 -12.560 1.00 41.36  C1
ATOM 2993 CD2 HIS 444  60.434 46.664 -12.075 1.00 41.40  C1
ATOM 2994 ND1 HIS 444  58.811 47.563 -13.261 1.00 41.74  C1
ATOM 2995 HD1 HIS 444  57.892 47.890 -13.410 1.00 0.00  C1
ATOM 2996 CE1 HIS 444  59.850 48.372 -13.217 1.00 42.00  C1
ATOM 2997 NE2 HIS 444  60.817 47.832 -12.502 1.00 41.38  C1
ATOM 2998 HE2 HIS 444  61.690 48.248 -12.334 1.00 0.00   C1
ATOM 2999 C  HIS 444  56.889 43.871 -10.878 1.00 40.10  C1
ATOM 3000 O  HIS 444  57.461 42.867 -11.309 1.00 40.15  C1
ATOM 3001 N  PRO 445  55.615 43.752 -10.406 1.00 42.06  C1
ATOM 3002 CD PRO 445  54.738 44.836 -9.937 1.00 41.56  C1
ATOM 3003 CA PRO 445  54.913 42.497 -10.276 1.00 40.90  C1
ATOM 3004 CB PRO 445  53.569 42.882 -9.730 1.00 39.35  C1
ATOM 3005 CG PRO 445  53.364 44.274 -10.215 1.00 39.35  C1
ATOM 3006 C  PRO 445  54.868 41.782 -11.600 1.00 42.18  C1
ATOM 3007 O  PRO 445  54.769 40.571 -11.569 1.00 45.69  C1
ATOM 3008 N  GLU 446  55.082 42.380 -12.769 1.00 41.64  C1
ATOM 3009 H  GLU 446  55.320 43.320 -12.761 1.00 0.00   C1
ATOM 3010 CA GLU 446  55.025 41.656 -14.029 1.00 42.05  C1
ATOM 3011 CB GLU 446  54.967 42.639 -15.183 1.00 47.06  C1
ATOM 3012 CG GLU 446  54.109 43.925 -14.992 1.00 56.71  C1
ATOM 3013 CD GLU 446  54.728 45.083 -14.162 1.00 62.28  C1
ATOM 3014 OE1 GLU 446  54.100 45.472 -13.178 1.00 66.26  C1
ATOM 3015 OE2 GLU 446  55.818 45.604 -14.473 1.00 65.55  C1
ATOM 3016 C  GLU 446  56.237 40.722 -14.197 1.00 40.44  C1
ATOM 3017 O  GLU 446  56.186 39.708 -14.904 1.00 41.66  C1
ATOM 3018 N  GLU 447  57.360 40.995 -13.538 1.00 37.89  C1
ATOM 3019 H  GLU 447  57.394 41.809 -12.999 1.00 0.00   C1
ATOM 3020 CA GLU 447  58.519 40.096 -13.509 1.00 36.73  C1
ATOM 3021 CB GLU 447  59.750 40.810 -12.976 1.00 34.60  C1
ATOM 3022 CG GLU 447  60.320 41.883 -13.850 1.00 35.27  C1
ATOM 3023 CD GLU 447  61.450 42.699 -13.197 1.00 36.14  C1
ATOM 3024 OE1 GLU 447  62.240 43.286 -13.939 1.00 37.31  C1
ATOM 3025 OE2 GLU 447  61.541 42.782 -11.970 1.00 32.80  C1
ATOM 3026 C  GLU 447  58.311 38.850 -12.599 1.00 36.31  C1
ATOM 3027 O  GLU 447  59.113 37.911 -12.592 1.00 36.33  C1
ATOM 3028 N  LEU 448  57.273 38.765 -11.769 1.00 33.81  C1
ATOM 3029 H  LEU 448  56.554 39.431 -11.802 1.00 0.00   C1
ATOM 3030 CA LEU 448  57.145 37.691 -10.839 1.00 31.88  C1
ATOM 3031 CB LEU 448  57.080 38.299 -9.484 1.00 29.29  C1
ATOM 3032 CG LEU 448  58.008 39.432 -9.140 1.00 29.81  C1
ATOM 3033 CD1 LEU 448  57.907 39.863 -7.684 1.00 26.02  C1
ATOM 3034 CD2 LEU 448  59.396 38.931 -9.392 1.00 31.13  C1
ATOM 3035 C  LEU 448  55.863 36.977 -11.165 1.00 33.75  C1
ATOM 3036 O  LEU 448  55.436 36.145 -10.382 1.00 33.96  C1
ATOM 3037 N  VAL 449  55.166 37.233 -12.263 1.00 36.99  C1
ATOM 3038 H  VAL 449  55.580 37.800 -12.942 1.00 0.00   C1
ATOM 3039 CA VAL 449  53.819 36.701 -12.472 1.00 41.46  C1
ATOM 3040 CB VAL 449  53.157 37.546 -13.625 1.00 41.56  C1
ATOM 3041 CG1 VAL 449  54.002 37.614 -14.880 1.00 42.22  C1
ATOM 3042 CG2 VAL 449  51.921 36.858 -14.112 1.00 42.01  C1
ATOM 3043 C  VAL 449  53.760 35.192 -12.733 1.00 44.81  C1
ATOM 3044 O  VAL 449  52.866 34.469 -12.227 1.00 44.54  C1
ATOM 3045 N  LEU 450  54.716 34.669 -13.515 1.00 47.21  C1
ATOM 3046 H  LEU 450  55.416 35.260 -13.870 1.00 0.00   C1
ATOM 3047 CA LEU 450  54.771 33.243 -13.781 1.00 50.57  C1
ATOM 3048 CB LEU 450  55.942 32.894 -14.628 1.00 50.75  C1
ATOM 3049 CG LEU 450  56.148 33.488 -15.994 1.00 52.39  C1
ATOM 3050 CD1 LEU 450  57.152 32.586 -16.673 1.00 53.05  C1
ATOM 3051 CD2 LEU 450  54.882 33.534 -16.833 1.00 54.10  C1
ATOM 3052 C  LEU 450  54.911 32.468 -12.471 1.00 53.84  C1
ATOM 3053 O  LEU 450  54.297 31.406 -12.266 1.00 55.62  C1
ATOM 3054 N  LEU 451  55.685 33.097 -11.575 1.00 55.46  C1
ATOM 3055 H  LEU 451  56.073 33.954 -11.849 1.00 0.00   C1
ATOM 3056 CA LEU 451  55.998 32.654 -10.223 1.00 56.01  C1
ATOM 3057 CB LEU 451  57.137 33.542 -9.731 1.00 55.80  C1
ATOM 3058 CG LEU 451  57.745 33.278 -8.394 1.00 56.96  C1
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FIGURE 5

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ATOM  3059 CD1 LEU  451      58.833  ..284  -8.653  1.00 59.12      C1
ATOM  3060 CD2 LEU  451      58.369  34.511  -7.751  1.00 58.27      C1
ATOM  3061  C  LEU  451      54.785  32.700  -9.280  1.00 55.96      C1
ATOM  3062  O  LEU  451      54.717  31.935  -8.319  1.00 53.74      C1
ATOM  3063  N  GLY  452      53.774  33.533  -9.522  1.00 57.52      C1
ATOM  3064  H  GLY  452      53.889  34.241 -10.191  1.00  0.00      C1
ATOM  3065 CA  GLY  452      52.567  33.515  -8.710  1.00 60.66      C1
ATOM  3066  C  GLY  452      51.942  32.137  -8.772  1.00 63.64      C1
ATOM  3067  O  GLY  452      51.476  31.593  -7.782  1.00 62.60      C1
ATOM  3068  N  HIS  453      52.089  31.545  -9.969  1.00 68.46      C1
ATOM  3069  H  HIS  453      52.628  32.040 -10.618  1.00  0.00      C1
ATOM  3070 CA  HIS  453      51.606  30.205 -10.326  1.00 72.27      C1
ATOM  3071 CB  HIS  453      51.785  29.908 -11.828  1.00 73.84      C1
ATOM  3072 CG  HIS  453      51.421  31.061 -12.777  1.00 77.81      C1
ATOM  3073 CD2 HIS  453      50.599  32.148 -12.498  1.00 79.29      C1
ATOM  3074 ND1 HIS  453      51.886  31.244 -14.012  1.00 79.84      C1
ATOM  3075 HD1 HIS  453      52.617  30.739 -14.425  1.00  0.00      C1
ATOM  3076 CE1 HIS  453      51.385  32.382 -14.470  1.00 81.11      C1
ATOM  3077 NE2 HIS  453      50.613  32.923 -13.551  1.00 79.85      C1
ATOM  3078 HE2 HIS  453      50.230  33.825 -13.586  1.00  0.00      C1
ATOM  3079  C  HIS  453      52.454  29.235  -9.515  1.00 73.43      C1
ATOM  3080  O  HIS  453      51.875  28.531  -8.692  1.00 73.56      C1
ATOM  3081  N  SER  454      53.785  29.207  -9.651  1.00 74.64      C1
ATOM  3082  H  SER  454      54.214  29.739 -10.351  1.00  0.00      C1
ATOM  3083 CA  SER  454      54.639  28.411  -8.765  1.00 77.07      C1
ATOM  3084 CB  SER  454      56.123  28.762  -8.980  1.00 77.34      C1
ATOM  3085 OG  SER  454      57.095  27.715  -9.124  1.00 75.28      C1
ATOM  3086 HG  SER  454      57.149  27.211  -8.306  1.00  0.00      C1
ATOM  3087  C  SER  454      54.332  28.608  -7.262  1.00 78.84      C1
ATOM  3088  O  SER  454      54.270  27.617  -6.535  1.00 80.57      C1
ATOM  3089  N  LEU  455      54.070  29.789  -6.693  1.00 79.72      C1
ATOM  3090  H  LEU  455      53.956  30.582  -7.250  1.00  0.00      C1
ATOM  3091 CA  LEU  455      53.849  29.915  -5.257  1.00 80.43      C1
ATOM  3092 CB  LEU  455      54.085  31.347  -4.838  1.00 80.20      C1
ATOM  3093 CG  LEU  455      55.389  31.981  -5.269  1.00 81.67      C1
ATOM  3094 CD1 LEU  455      55.254  33.494  -5.419  1.00 81.36      C1
ATOM  3095 CD2 LEU  455      56.431  31.579  -4.264  1.00 82.26      C1
ATOM  3096  C  LEU  455      52.438  29.510  -4.848  1.00 81.56      C1
ATOM  3097  O  LEU  455      52.038  29.893  -3.741  1.00 82.22      C1
ATOM  3098  N  GLY  456      51.653  28.816  -5.708  1.00 81.89      C1
ATOM  3099  H  GLY  456      52.026  28.592  -6.584  1.00  0.00      C1
ATOM  3100 CA  GLY  456      50.269  28.361  -5.467  1.00 82.22      C1
ATOM  3101  C  GLY  456      49.220  29.386  -4.973  1.00 82.56      C1
ATOM  3102  O  GLY  456      48.268  28.989  -4.276  1.00 82.38      C1
ATOM  3103  N  ILE  457      49.342  30.697  -5.286  1.00 82.54      C1
ATOM  3104  H  ILE  457      50.075  30.942  -5.894  1.00  0.00      C1
ATOM  3105 CA  ILE  457      48.435  31.761  -4.824  1.00 81.63      C1
ATOM  3106 CB  ILE  457      49.110  33.157  -5.086  1.00 80.69      C1
ATOM  3107 CG2 ILE  457      48.218  34.305  -4.662  1.00 79.76      C1
ATOM  3108 CG1 ILE  457      50.369  33.275  -4.253  1.00 79.82      C1
ATOM  3109 CD  ILE  457      51.506  33.868  -5.081  1.00 77.89      C1
ATOM  3110  C  ILE  457      47.048  31.698  -5.472  1.00 81.70      C1
ATOM  3111  O  ILE  457      46.903  31.761  -6.700  1.00 82.57      C1
ATOM  3112  N  PRO  458      45.963  31.583  -4.705  1.00 82.40      C1
ATOM  3113 CD  PRO  458      45.959  31.225  -3.278  1.00 81.21      C1
ATOM  3114 CA  PRO  458      44.607  31.643  -5.264  1.00 80.74      C1
ATOM  3115 CB  PRO  458      43.779  30.942  -4.157  1.00 81.12      C1
ATOM  3116 CG  PRO  458      44.757  30.293  -3.173  1.00 80.47      C1
ATOM  3117  C  PRO  458      44.120  33.063  -5.648  1.00 79.70      C1
ATOM  3118  O  PRO  458      43.674  33.736  -4.718  1.00 80.10      C1
ATOM  3119  N  TRP  459      44.171  33.662  -6.861  1.00 78.19      C1
ATOM  3120  H  TRP  459      44.614  33.185  -7.591  1.00  0.00      C1
ATOM  3121 CA  TRP  459      43.543  34.986  -7.092  1.00 77.73      C1
ATOM  3122 CB  TRP  459      43.802  35.428  -8.522  1.00 78.71      C1
ATOM  3123 CG  TRP  459      43.054  36.677  -9.017  1.00 81.37      C1
ATOM  3124 CD2 TRP  459      41.802  36.771  -9.618  1.00 82.89      C1
ATOM  3125 CE2 TRP  459      41.717  38.139  -9.883  1.00 84.21      C1
ATOM  3126 CE3 TRP  459      40.738  35.960  -9.983  1.00 84.28      C1
ATOM  3127 CD1 TRP  459      43.661  37.899  -8.925  1.00 83.89      C1
ATOM  3128 NE1 TRP  459      42.828  38.765  -9.460  1.00 85.23      C1
ATOM  3129 HE1 TRP  459      42.944  39.738  -9.483  1.00  0.00      C1
ATOM  3130 CZ2 TRP  459      40.615  38.727 -10.494  1.00 84.17      C1
ATOM  3131 CZ3 TRP  459      39.630  36.538 -10.597  1.00 84.56      C1
ATOM  3132 CH2 TRP  459      39.562  37.904 -10.852  1.00 84.83      C1
ATOM  3133  C  TRP  459      42.009  35.013  -6.827  1.00 77.41      C1
ATOM  3134  O  TRP  459      41.202  34.244  -7.376  1.00 76.38      C1
ATOM  3135  N  ALA  460      41.557  35.969  -6.020  1.00 76.81      C1
ATOM  3136  H  ALA  460      42.187  36.640  -5.689  1.00  0.00      C1
ATOM  3137 CA  ALA  460      40.158  36.044  -5.613  1.00 76.44      C1
ATOM  3138 CB  ALA  460      40.072  36.724  -4.243  1.00 75.51      C1
ATOM  3139  C  ALA  460      39.237  36.784  -6.588  1.00 76.29      C1
ATOM  3140  O  ALA  460      39.449  37.976  -6.833  1.00 76.98      C1
ATOM  3141  N  PRO  461      38.217  36.147  -7.187  1.00 76.26      C1
ATOM  3142 CD  PRO  461      38.104  34.684  -7.245  1.00 75.88      C1
ATOM  3143 CA  PRO  461      37.242  36.793  -8.068  1.00 75.46      C1
ATOM  3144 CB  PRO  461      36.605  35.605  -8.755  1.00 75.71      C1
ATOM  3145 CG  PRO  461      36.703  34.458  -7.767  1.00 75.60      C1
ATOM  3146  C  PRO  461      36.221  37.803  -7.545  1.00 75.72      C1
ATOM  3147  O  PRO  461      35.677  37.734  -6.440  1.00 73.66      C1
ATOM  3148  N  LEU  462      35.996  38.767  -8.449  1.00 77.19      C1
ATOM  3149  H  LEU  462      36.516  38.723  -9.277  1.00  0.00      C1
ATOM  3150 CA  LEU  462      35.069  39.891  -8.275  1.00 78.87      C1
ATOM  3151 CB  LEU  462      35.674  40.984  -7.360  1.00 78.32      C1
ATOM  3152 CG  LEU  462      34.786  41.959  -6.558  1.00 78.09      C1
ATOM  3153 CD1 LEU  462      34.051  42.987  -7.406  1.00 78.32      C1
ATOM  3154 CD2 LEU  462      33.767  41.092  -5.828  1.00 78.62      C1
ATOM  3155  C  LEU  462      34.701  40.565  -9.611  1.00 80.64      C1
ATOM  3156 OT1 LEU  462      33.507  40.842  -9.808  1.00 81.74      C1
ATOM  3157 OT2 LEU  462      35.606  40.847 -10.417  1.00 81.59      C1
ATOM  3158 CB  LEU  472      22.074  42.654  -1.426  1.00 62.24      C2
ATOM  3159 CG  LEU  472      22.278  44.145  -1.189  1.00 59.58      C2
ATOM  3160 CD1 LEU  472      23.496  44.325  -0.328  1.00 59.14      C2
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FIGURE 5

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ATOM  3161 CD2 LEU  472      22.501  -4.883  -2.486  1.00 56.85      C2
ATOM  3162 C   LEU  472      23.504  40.625  -1.996  1.00 63.91      C2
ATOM  3163 O   LEU  472      23.738  39.874  -2.949  1.00 64.90      C2
ATOM  3164 HT1 LEU  472      21.563  41.441  -3.595  1.00  0.00      C2
ATOM  3165 HT2 LEU  472      23.091  41.291  -4.237  1.00  0.00      C2
ATOM  3166 N   LEU  472      22.472  41.930  -3.693  1.00 64.29      C2
ATOM  3167 HT3 LEU  472      22.358  42.849  -4.160  1.00  0.00      C2
ATOM  3168 CA  LEU  472      23.092  42.037  -2.386  1.00 63.85      C2
ATOM  3169 N   ALA  473      23.652  40.229  -0.733  1.00 63.02      C2
ATOM  3170 H   ALA  473      23.533  40.867   0.002  1.00  0.00      C2
ATOM  3171 CA  ALA  473      24.023  38.881  -0.353  1.00 62.37      C2
ATOM  3172 CB  ALA  473      22.870  37.939  -0.558  1.00 63.65      C2
ATOM  3173 C   ALA  473      25.196  38.354  -1.126  1.00 62.01      C2
ATOM  3174 O   ALA  473      26.301  38.651  -0.715  1.00 63.36      C2
ATOM  3175 N   GLY  474      25.032  37.784  -2.306  1.00 61.43      C2
ATOM  3176 H   GLY  474      24.148  37.818  -2.722  1.00  0.00      C2
ATOM  3177 CA  GLY  474      26.101  37.137  -3.047  1.00 63.80      C2
ATOM  3178 C   GLY  474      27.354  37.950  -3.356  1.00 65.13      C2
ATOM  3179 O   GLY  474      28.482  37.417  -3.257  1.00 66.24      C2
ATOM  3180 N   CYS  475      27.175  39.237  -3.757  1.00 64.88      C2
ATOM  3181 H   CYS  475      26.261  39.550  -3.885  1.00  0.00      C2
ATOM  3182 CA  CYS  475      28.308  40.127  -4.068  1.00 61.84      C2
ATOM  3183 CB  CYS  475      27.925  41.413  -4.806  1.00 63.74      C2
ATOM  3184 SG  CYS  475      29.494  42.075  -5.437  1.00 68.86      C2
ATOM  3185 C   CYS  475      28.995  40.567  -2.795  1.00 57.30      C2
ATOM  3186 O   CYS  475      30.214  40.449  -2.724  1.00 57.14      C2
ATOM  3187 N   LEU  476      28.230  40.983  -1.779  1.00 53.29      C2
ATOM  3188 H   LEU  476      27.264  41.024  -1.885  1.00  0.00      C2
ATOM  3189 CA  LEU  476      28.797  41.315  -0.493  1.00 50.43      C2
ATOM  3190 CB  LEU  476      27.719  41.723   0.523  1.00 45.68      C2
ATOM  3191 CG  LEU  476      27.130  43.165   0.497  1.00 42.80      C2
ATOM  3192 CD1 LEU  476      26.670  43.559   1.896  1.00 36.25      C2
ATOM  3193 CD2 LEU  476      28.180  44.180   0.057  1.00 40.22      C2
ATOM  3194 C   LEU  476      29.546  40.108   0.042  1.00 50.42      C2
ATOM  3195 O   LEU  476      30.614  40.222   0.646  1.00 50.61      C2
ATOM  3196 N   SER  477      29.053  38.922  -0.270  1.00 50.62      C2
ATOM  3197 H   SER  477      28.196  38.860  -0.729  1.00  0.00      C2
ATOM  3198 CA  SER  477      29.721  37.712   0.125  1.00 51.41      C2
ATOM  3199 CB  SER  477      28.778  36.524  -0.051  1.00 53.45      C2
ATOM  3200 OG  SER  477      27.732  36.616   0.926  1.00 57.65      C2
ATOM  3201 HG  SER  477      27.280  37.462   0.828  1.00  0.00      C2
ATOM  3202 C   SER  477      30.978  37.525  -0.681  1.00 50.75      C2
ATOM  3203 O   SER  477      31.980  37.143  -0.068  1.00 51.41      C2
ATOM  3204 N   GLN  478      31.037  37.788  -1.984  1.00 50.21      C2
ATOM  3205 H   GLN  478      30.222  38.056  -2.457  1.00  0.00      C2
ATOM  3206 CA  GLN  478      32.307  37.697  -2.715  1.00 51.37      C2
ATOM  3207 CB  GLN  478      32.064  37.929  -4.166  1.00 53.65      C2
ATOM  3208 CG  GLN  478      31.983  36.570  -4.788  1.00 57.32      C2
ATOM  3209 CD  GLN  478      31.354  36.649  -6.160  1.00 60.47      C2
ATOM  3210 OE1 GLN  478      31.999  36.504  -7.205  1.00 62.26      C2
ATOM  3211 NE2 GLN  478      30.045  36.878  -6.167  1.00 62.16      C2
ATOM  3212 HE21 GLN  478      29.569  36.972  -5.317  1.00  0.00      C2
ATOM  3213 HE22 GLN  478      29.641  36.928  -7.054  1.00  0.00      C2
ATOM  3214 C   GLN  478      33.398  38.670  -2.249  1.00 50.66      C2
ATOM  3215 O   GLN  478      34.584  38.314  -2.217  1.00 50.13      C2
ATOM  3216 N   LEU  479      33.045  39.909  -1.859  1.00 48.78      C2
ATOM  3217 H   LEU  479      32.131  40.223  -2.039  1.00  0.00      C2
ATOM  3218 CA  LEU  479      34.015  40.800  -1.235  1.00 45.87      C2
ATOM  3219 CB  LEU  479      33.434  42.141  -0.827  1.00 47.03      C2
ATOM  3220 CG  LEU  479      32.853  43.083  -1.818  1.00 49.40      C2
ATOM  3221 CD1 LEU  479      32.596  44.393  -1.078  1.00 48.15      C2
ATOM  3222 CD2 LEU  479      33.779  43.258  -3.000  1.00 48.59      C2
ATOM  3223 C   LEU  479      34.505  40.146   0.056  1.00 42.13      C2
ATOM  3224 O   LEU  479      35.695  39.955   0.262  1.00 40.90      C2
ATOM  3225 N   HIS  480      33.609  39.766   0.950  1.00 39.56      C2
ATOM  3226 H   HIS  480      32.658  39.935   0.763  1.00  0.00      C2
ATOM  3227 CA  HIS  480      33.979  39.108   2.179  1.00 37.81      C2
ATOM  3228 CB  HIS  480      32.742  38.714   2.922  1.00 34.29      C2
ATOM  3229 CG  HIS  480      33.094  38.241   4.309  1.00 33.82      C2
ATOM  3230 CD2 HIS  480      33.123  36.932   4.709  1.00 33.44      C2
ATOM  3231 ND1 HIS  480      33.450  38.995   5.344  1.00 34.27      C2
ATOM  3232 HD1 HIS  480      33.505  39.976   5.362  1.00  0.00      C2
ATOM  3233 CE1 HIS  480      33.706  38.223   6.365  1.00 33.80      C2
ATOM  3234 NE2 HIS  480      33.504  36.986   5.965  1.00 37.12      C2
ATOM  3235 HE2 HIS  480      33.637  36.202   6.544  1.00  0.00      C2
ATOM  3236 C   HIS  480      34.836  37.860   1.961  1.00 39.08      C2
ATOM  3237 O   HIS  480      35.716  37.631   2.791  1.00 40.93      C2
ATOM  3238 N   SER  481      34.615  37.029   0.935  1.00 39.24      C2
ATOM  3239 H   SER  481      33.900  37.241   0.305  1.00  0.00      C2
ATOM  3240 CA  SER  481      35.391  35.818   0.683  1.00 38.17      C2
ATOM  3241 CB  SER  481      34.813  34.943  -0.420  1.00 40.42      C2
ATOM  3242 OG  SER  481      33.454  34.597  -0.137  1.00 47.61      C2
ATOM  3243 HG  SER  481      32.898  35.385  -0.162  1.00  0.00      C2
ATOM  3244 C   SER  481      36.724  36.272   0.211  1.00 36.12      C2
ATOM  3245 O   SER  481      37.692  35.793   0.765  1.00 36.23      C2
ATOM  3246 N   GLY  482      36.786  37.206  -0.744  1.00 36.21      C2
ATOM  3247 H   GLY  482      35.956  37.498  -1.168  1.00  0.00      C2
ATOM  3248 CA  GLY  482      38.028  37.792  -1.266  1.00 36.50      C2
ATOM  3249 C   GLY  482      38.958  38.296  -0.151  1.00 36.14      C2
ATOM  3250 O   GLY  482      40.142  37.936  -0.055  1.00 36.65      C2
ATOM  3251 N   LEU  483      38.381  39.084   0.750  1.00 34.64      C2
ATOM  3252 H   LEU  483      37.445  39.326   0.608  1.00  0.00      C2
ATOM  3253 CA  LEU  483      39.073  39.593   1.900  1.00 32.07      C2
ATOM  3254 CB  LEU  483      38.134  40.442   2.731  1.00 31.17      C2
ATOM  3255 CG  LEU  483      37.535  41.687   2.081  1.00 31.11      C2
ATOM  3256 CD1 LEU  483      36.757  42.411   3.156  1.00 30.82      C2
ATOM  3257 CD2 LEU  483      38.599  42.593   1.480  1.00 29.56      C2
ATOM  3258 C   LEU  483      39.600  38.461   2.745  1.00 32.91      C2
ATOM  3259 O   LEU  483      40.752  38.498   3.199  1.00 31.25      C2
ATOM  3260 N   PHE  484      38.767  37.422   2.925  1.00 34.06      C2
ATOM  3261 H   PHE  484      37.930  37.408   2.471  1.00  0.00      C2
ATOM  3262 CA  PHE  484      39.105  36.298   3.788  1.00 34.60      C2
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FIGURE 5

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ATOM  3263  CB  PHE  484      37.975  35.300   3.925  1.00 37.46      C2
ATOM  3264  CG  PHE  484      38.268  34.183   4.897  1.00 40.86      C2
ATOM  3265  CD1 PHE  484      38.219  32.884   4.482  1.00 45.62      C2
ATOM  3266  CD2 PHE  484      38.528  34.445   6.210  1.00 43.62      C2
ATOM  3267  CE1 PHE  484      38.421  31.858   5.395  1.00 47.98      C2
ATOM  3268  CE2 PHE  484      38.731  33.427   7.119  1.00 46.78      C2
ATOM  3269  CZ  PHE  484      38.677  32.119   6.720  1.00 48.06      C2
ATOM  3270  C   PHE  484      40.245  35.602   3.113  1.00 33.92      C2
ATOM  3271  O   PHE  484      41.162  35.289   3.826  1.00 34.25      C2
ATOM  3272  N   LEU  485      40.326  35.413   1.799  1.00 32.75      C2
ATOM  3273  H   LEU  485      39.577  35.717   1.250  1.00  0.00      C2
ATOM  3274  CA  LEU  485      41.475  34.778   1.163  1.00 33.74      C2
ATOM  3275  CB  LEU  485      41.183  34.629  -0.305  1.00 35.35      C2
ATOM  3276  CG  LEU  485      42.101  33.962  -1.275  1.00 37.80      C2
ATOM  3277  CD1 LEU  485      41.181  33.404  -2.345  1.00 41.44      C2
ATOM  3278  CD2 LEU  485      43.125  34.903  -1.899  1.00 40.07      C2
ATOM  3279  C   LEU  485      42.740  35.585   1.376  1.00 33.95      C2
ATOM  3280  O   LEU  485      43.766  35.060   1.850  1.00 33.84      C2
ATOM  3281  N   TYR  486      42.609  36.885   1.034  1.00 33.67      C2
ATOM  3282  H   TYR  486      41.757  37.186   0.659  1.00  0.00      C2
ATOM  3283  CA  TYR  486      43.662  37.862   1.242  1.00 31.33      C2
ATOM  3284  CB  TYR  486      43.210  39.290   0.714  1.00 35.33      C2
ATOM  3285  CG  TYR  486      43.300  39.325  -0.825  1.00 33.37      C2
ATOM  3286  CD1 TYR  486      42.154  39.405  -1.579  1.00 32.79      C2
ATOM  3287  CE1 TYR  486      42.228  39.290  -2.944  1.00 33.73      C2
ATOM  3288  CD2 TYR  486      44.533  39.153  -1.445  1.00 34.59      C2
ATOM  3289  CE2 TYR  486      44.618  39.033  -2.818  1.00 34.63      C2
ATOM  3290  CZ  TYR  486      43.451  39.096  -3.562  1.00 35.58      C2
ATOM  3291  OH  TYR  486      43.484  38.880  -4.942  1.00 38.24      C2
ATOM  3292  HH  TYR  486      42.614  39.086  -5.306  1.00  0.00      C2
ATOM  3293  C   TYR  486      44.068  37.905   2.697  1.00 27.39      C2
ATOM  3294  O   TYR  486      45.258  38.007   2.942  1.00 26.06      C2
ATOM  3295  N   GLN  487      43.270  37.691   3.708  1.00 26.95      C2
ATOM  3296  H   GLN  487      42.315  37.545   3.565  1.00  0.00      C2
ATOM  3297  CA  GLN  487      43.835  37.646   5.031  1.00 28.33      C2
ATOM  3298  CB  GLN  487      42.690  37.578   6.050  1.00 32.66      C2
ATOM  3299  CG  GLN  487      43.092  37.979   7.485  1.00 37.50      C2
ATOM  3300  CD  GLN  487      43.966  39.252   7.469  1.00 40.54      C2
ATOM  3301  OE1 GLN  487      43.441  40.346   7.292  1.00 40.45      C2
ATOM  3302  NE2 GLN  487      45.305  39.206   7.549  1.00 38.19      C2
ATOM  3303 HE21 GLN  487      45.755  40.057   7.452  1.00  0.00      C2
ATOM  3304 HE22 GLN  487      45.736  38.340   7.702  1.00  0.00      C2
ATOM  3305  C   GLN  487      44.791  36.455   5.207  1.00 28.53      C2
ATOM  3306  O   GLN  487      45.774  36.542   5.964  1.00 28.72      C2
ATOM  3307  N   GLY  488      44.550  35.363   4.454  1.00 28.32      C2
ATOM  3308  H   GLY  488      43.799  35.400   3.824  1.00  0.00      C2
ATOM  3309  CA  GLY  488      45.291  34.120   4.557  1.00 26.04      C2
ATOM  3310  C   GLY  488      46.660  34.264   4.033  1.00 25.75      C2
ATOM  3311  O   GLY  488      47.660  33.946   4.712  1.00 25.86      C2
ATOM  3312  N   LEU  489      46.655  34.798   2.818  1.00 25.05      C2
ATOM  3313  H   LEU  489      45.798  35.062   2.416  1.00  0.00      C2
ATOM  3314  CA  LEU  489      47.911  34.990   2.099  1.00 25.63      C2
ATOM  3315  CB  LEU  489      47.708  35.570   0.725  1.00 27.66      C2
ATOM  3316  CG  LEU  489      46.761  34.755  -0.189  1.00 30.83      C2
ATOM  3317  CD1 LEU  489      46.373  35.506  -1.471  1.00 30.43      C2
ATOM  3318  CD2 LEU  489      47.472  33.454  -0.502  1.00 32.62      C2
ATOM  3319  C   LEU  489      48.783  35.936   2.853  1.00 25.28      C2
ATOM  3320  O   LEU  489      49.973  35.705   2.914  1.00 27.37      C2
ATOM  3321  N   LEU  490      48.237  36.935   3.534  1.00 25.79      C2
ATOM  3322  H   LEU  490      47.267  37.079   3.515  1.00  0.00      C2
ATOM  3323  CA  LEU  490      49.072  37.868   4.220  1.00 25.96      C2
ATOM  3324  CB  LEU  490      48.274  39.139   4.567  1.00 27.96      C2
ATOM  3325  CG  LEU  490      47.823  40.131   3.474  1.00 27.89      C2
ATOM  3326  CD1 LEU  490      46.772  41.019   4.123  1.00 28.63      C2
ATOM  3327  CD2 LEU  490      48.988  40.942   2.899  1.00 28.15      C2
ATOM  3328  C   LEU  490      49.619  37.243   5.459  1.00 27.33      C2
ATOM  3329  O   LEU  490      50.740  37.528   5.865  1.00 26.73      C2
ATOM  3330  N   GLN  491      48.883  36.370   6.111  1.00 29.88      C2
ATOM  3331  H   GLN  491      47.984  36.127   5.799  1.00  0.00      C2
ATOM  3332  CA  GLN  491      49.430  35.809   7.314  1.00 33.01      C2
ATOM  3333  CB  GLN  491      48.305  35.113   8.027  1.00 38.68      C2
ATOM  3334  CG  GLN  491      47.856  35.963   9.197  1.00 46.07      C2
ATOM  3335  CD  GLN  491      46.348  36.262   9.278  1.00 50.83      C2
ATOM  3336  OE1 GLN  491      45.965  37.436   9.402  1.00 51.92      C2
ATOM  3337  NE2 GLN  491      45.425  35.294   9.278  1.00 51.67      C2
ATOM  3338 HE21 GLN  491      45.723  34.353   9.288  1.00  0.00      C2
ATOM  3339 HE22 GLN  491      44.489  35.560   9.286  1.00  0.00      C2
ATOM  3340  C   GLN  491      50.582  34.867   6.986  1.00 33.58      C2
ATOM  3341  O   GLN  491      51.582  34.828   7.715  1.00 34.65      C2
ATOM  3342  N   ALA  492      50.482  34.191   5.824  1.00 34.15      C2
ATOM  3343  H   ALA  492      49.701  34.382   5.264  1.00  0.00      C2
ATOM  3344  CA  ALA  492      51.416  33.177   5.321  1.00 33.64      C2
ATOM  3345  CB  ALA  492      50.818  32.500   4.081  1.00 31.67      C2
ATOM  3346  C   ALA  492      52.802  33.678   4.959  1.00 34.79      C2
ATOM  3347  O   ALA  492      53.789  32.943   4.879  1.00 36.03      C2
ATOM  3348  N   LEU  493      52.885  34.981   4.728  1.00 35.94      C2
ATOM  3349  H   LEU  493      52.060  35.510   4.721  1.00  0.00      C2
ATOM  3350  CA  LEU  493      54.139  35.634   4.426  1.00 34.86      C2
ATOM  3351  CB  LEU  493      53.898  36.990   3.747  1.00 31.36      C2
ATOM  3352  CG  LEU  493      53.127  37.065   2.443  1.00 28.27      C2
ATOM  3353  CD1 LEU  493      52.715  38.495   2.214  1.00 31.74      C2
ATOM  3354  CD2 LEU  493      53.977  36.608   1.285  1.00 28.79      C2
ATOM  3355  C   LEU  493      54.879  35.843   5.721  1.00 36.15      C2
ATOM  3356  O   LEU  493      55.985  36.374   5.694  1.00 36.70      C2
ATOM  3357  N   GLU  494      54.300  35.497   6.855  1.00 38.35      C2
ATOM  3358  H   GLU  494      53.395  35.130   6.836  1.00  0.00      C2
ATOM  3359  CA  GLU  494      54.910  35.648   8.157  1.00 43.14      C2
ATOM  3360  CB  GLU  494      55.621  34.340   8.545  1.00 46.61      C2
ATOM  3361  CG  GLU  494      54.711  33.471   9.419  1.00 53.71      C2
ATOM  3362  CD  GLU  494      54.195  32.160   8.785  1.00 60.27      C2
ATOM  3363  OE1 GLU  494      53.146  31.653   9.230  1.00 64.52      C2
ATOM  3364  OE2 GLU  494      54.839  31.630   7.862  1.00 62.76      C2
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FIGURE 5

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ATOM 3365 C  GLU 494    55.865 36.825  8.343 1.00 44.32      C2
ATOM 3366 O  GLU 494    57.055 36.678  8.610 1.00 46.91      C2
ATOM 3367 N  GLY 495    55.358 38.046  8.114 1.00 44.32      C2
ATOM 3368 H  GLY 495    54.450 38.112  7.753 1.00  0.00      C2
ATOM 3369 CA GLY 495    56.104 39.272  8.368 1.00 42.36      C2
ATOM 3370 C  GLY 495    57.015 39.695  7.238 1.00 42.33      C2
ATOM 3371 O  GLY 495    57.397 40.866  7.220 1.00 42.42      C2
ATOM 3372 N  ILE 496    57.310 38.802  6.279 1.00 41.04      C2
ATOM 3373 H  ILE 496    56.927 37.906  6.374 1.00  0.00      C2
ATOM 3374 CA ILE 496    58.259 38.993  5.192 1.00 41.15      C2
ATOM 3375 CB ILE 496    57.929 40.216  4.253 1.00 38.60      C2
ATOM 3376 CG2 ILE 496   59.077 40.437  3.248 1.00 37.62      C2
ATOM 3377 CG1 ILE 496   56.662 39.964  3.480 1.00 36.39      C2
ATOM 3378 CD ILE 496    56.314 41.071  2.470 1.00 35.27      C2
ATOM 3379 C  ILE 496    59.672 39.203  5.749 1.00 42.91      C2
ATOM 3380 O  ILE 496    60.541 38.396  5.448 1.00 44.22      C2
ATOM 3381 N  SER 497    59.998 40.228  6.533 1.00 44.31      C2
ATOM 3382 H  SER 497    59.297 40.852  6.827 1.00  0.00      C2
ATOM 3383 CA SER 497    61.346 40.501  6.992 1.00 44.86      C2
ATOM 3384 CB SER 497    62.204 41.254  5.938 1.00 44.13      C2
ATOM 3385 OG SER 497    62.181 42.673  6.033 1.00 40.74      C2
ATOM 3386 HG SER 497    62.531 42.964  5.170 1.00  0.00      C2
ATOM 3387 C  SER 497    61.164 41.413  8.185 1.00 45.85      C2
ATOM 3388 O  SER 497    60.132 42.110  8.288 1.00 47.55      C2
ATOM 3389 N  PRO 498    62.164 41.490  9.071 1.00 44.96      C2
ATOM 3390 CD PRO 498    63.338 40.621  9.126 1.00 42.33      C2
ATOM 3391 CA PRO 498    62.086 42.327 10.250 1.00 44.88      C2
ATOM 3392 CB PRO 498    63.431 42.038 10.885 1.00 45.13      C2
ATOM 3393 CG PRO 498    63.629 40.581 10.603 1.00 42.00      C2
ATOM 3394 C  PRO 498    61.760 43.799  9.983 1.00 45.22      C2
ATOM 3395 O  PRO 498    61.215 44.446 10.869 1.00 45.24      C2
ATOM 3396 N  GLU 499    62.017 44.314  8.777 1.00 46.16      C2
ATOM 3397 H  GLU 499    62.362 43.716  8.081 1.00  0.00      C2
ATOM 3398 CA GLU 499    61.731 45.699  8.391 1.00 48.06      C2
ATOM 3399 CB GLU 499    62.498 46.193  7.155 1.00 52.19      C2
ATOM 3400 CG GLU 499    64.001 46.187  7.100 1.00 57.51      C2
ATOM 3401 CD GLU 499    64.544 44.777  7.076 1.00 60.61      C2
ATOM 3402 OE1 GLU 499   64.755 44.231  8.162 1.00 62.96      C2
ATOM 3403 OE2 GLU 499   64.739 44.234  5.984 1.00 62.79      C2
ATOM 3404 C  GLU 499    60.269 45.896  7.981 1.00 46.94      C2
ATOM 3405 O  GLU 499    59.600 46.895  8.272 1.00 48.15      C2
ATOM 3406 N  LEU 500    59.806 44.934  7.193 1.00 44.38      C2
ATOM 3407 H  LEU 500    60.351 44.137  7.027 1.00  0.00      C2
ATOM 3408 CA LEU 500    58.491 44.997  6.651 1.00 41.08      C2
ATOM 3409 CB LEU 500    58.519 44.197  5.445 1.00 41.37      C2
ATOM 3410 CG LEU 500    59.303 44.862  4.351 1.00 42.70      C2
ATOM 3411 CD1 LEU 500   59.776 43.828  3.351 1.00 43.98      C2
ATOM 3412 CD2 LEU 500   58.427 45.874  3.671 1.00 45.04      C2
ATOM 3413 C  LEU 500    57.455 44.521  7.628 1.00 40.59      C2
ATOM 3414 O  LEU 500    56.274 44.835  7.463 1.00 40.69      C2
ATOM 3415 N  GLY 501    57.866 43.835  8.685 1.00 39.37      C2
ATOM 3416 H  GLY 501    58.808 43.579  8.730 1.00  0.00      C2
ATOM 3417 CA GLY 501    56.974 43.386  9.734 1.00 39.59      C2
ATOM 3418 C  GLY 501    55.816 44.324 10.092 1.00 39.66      C2
ATOM 3419 O  GLY 501    54.661 44.034  9.777 1.00 40.66      C2
ATOM 3420 N  PRO 502    55.986 45.462 10.742 1.00 39.90      C2
ATOM 3421 CD PRO 502    57.227 45.908 11.335 1.00 41.18      C2
ATOM 3422 CA PRO 502    54.912 46.387 11.045 1.00 38.67      C2
ATOM 3423 CB PRO 502    55.594 47.494 11.791 1.00 39.23      C2
ATOM 3424 CG PRO 502    56.989 47.405 11.221 1.00 41.36      C2
ATOM 3425 C  PRO 502    54.158 46.849  9.817 1.00 37.54      C2
ATOM 3426 O  PRO 502    52.966 47.139  9.961 1.00 38.36      C2
ATOM 3427 N  THR 503    54.728 46.887  8.609 1.00 35.13      C2
ATOM 3428 H  THR 503    55.663 46.638  8.449 1.00  0.00      C2
ATOM 3429 CA THR 503    53.940 47.283  7.462 1.00 35.09      C2
ATOM 3430 CB THR 503    54.832 47.376  6.245 1.00 34.48      C2
ATOM 3431 OG1 THR 503   56.025 48.018  6.668 1.00 38.23      C2
ATOM 3432 HG1 THR 503   55.857 48.946  6.845 1.00  0.00      C2
ATOM 3433 CG2 THR 503   54.197 48.162  5.126 1.00 35.56      C2
ATOM 3434 C  THR 503    52.836 46.252  7.215 1.00 35.37      C2
ATOM 3435 O  THR 503    51.671 46.552  6.915 1.00 37.11      C2
ATOM 3436 N  LEU 504    53.218 44.996  7.380 1.00 34.02      C2
ATOM 3437 H  LEU 504    54.146 44.799  7.647 1.00  0.00      C2
ATOM 3438 CA LEU 504    52.301 43.912  7.173 1.00 32.50      C2
ATOM 3439 CB LEU 504    53.127 42.650  7.002 1.00 34.78      C2
ATOM 3440 CG LEU 504    53.464 42.256  5.601 1.00 34.07      C2
ATOM 3441 CD1 LEU 504   54.163 40.977  5.667 1.00 37.97      C2
ATOM 3442 CD2 LEU 504   52.254 41.865  4.809 1.00 37.34      C2
ATOM 3443 C  LEU 504    51.324 43.821  8.328 1.00 29.54      C2
ATOM 3444 O  LEU 504    50.141 43.562  8.078 1.00 30.40      C2
ATOM 3445 N  ASP 505    51.736 44.106  9.551 1.00 26.09      C2
ATOM 3446 H  ASP 505    52.689 44.269  9.699 1.00  0.00      C2
ATOM 3447 CA ASP 505    50.798 44.084 10.643 1.00 27.88      C2
ATOM 3448 CB ASP 505    51.446 44.345 11.926 1.00 29.86      C2
ATOM 3449 CG ASP 505    52.500 43.312 12.239 1.00 34.64      C2
ATOM 3450 OD1 ASP 505   52.663 42.298 11.534 1.00 41.04      C2
ATOM 3451 OD2 ASP 505   53.179 43.542 13.224 1.00 37.40      C2
ATOM 3452 C  ASP 505    49.661 45.060 10.568 1.00 28.61      C2
ATOM 3453 O  ASP 505    48.566 44.739 11.039 1.00 30.30      C2
ATOM 3454 N  THR 506    49.894 46.242 10.002 1.00 28.29      C2
ATOM 3455 H  THR 506    50.823 46.493  9.804 1.00  0.00      C2
ATOM 3456 CA THR 506    48.860 47.225  9.731 1.00 25.74      C2
ATOM 3457 CB THR 506    49.497 48.556  9.336 1.00 26.14      C2
ATOM 3458 OG1 THR 506   49.944 49.099 10.588 1.00 31.63      C2
ATOM 3459 HG1 THR 506   49.243 49.072 11.246 1.00  0.00      C2
ATOM 3460 CG2 THR 506   48.594 49.517  8.619 1.00 24.46      C2
ATOM 3461 C  THR 506    48.022 46.735  8.615 1.00 24.00      C2
ATOM 3462 O  THR 506    46.817 46.864  8.719 1.00 25.85      C2
ATOM 3463 N  LEU 507    48.554 46.196  7.525 1.00 23.51      C2
ATOM 3464 H  LEU 507    49.527 46.073  7.453 1.00  0.00      C2
ATOM 3465 CA LEU 507    47.682 45.770  6.434 1.00 23.85      C2
ATOM 3466 CB LEU 507    48.574 45.408  5.196 1.00 25.33      C2
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FIGURE 5

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ATOM  3467 CG  LEU  S07    48.010  44.919   3.858  1.00 20.85      C2
ATOM  3468 CD1 LEU  S07    46.771  45.650   3.455  1.00 24.13      C2
ATOM  3469 CD2 LEU  S07    49.074  45.055   2.842  1.00 20.13      C2
ATOM  3470 C   LEU  S07    46.766  44.640   6.880  1.00 24.09      C2
ATOM  3471 O   LEU  S07    45.600  44.764   6.541  1.00 25.80      C2
ATOM  3472 N   GLN  S08    47.152  43.618   7.661  1.00 24.01      C2
ATOM  3473 H   GLN  S08    48.112  43.555   7.866  1.00  0.00      C2
ATOM  3474 CA  GLN  S08    46.228  42.625   8.214  1.00 23.71      C2
ATOM  3475 CB  GLN  S08    46.961  41.627   9.036  1.00 23.83      C2
ATOM  3476 CG  GLN  S08    47.937  40.899   8.173  1.00 31.64      C2
ATOM  3477 CD  GLN  S08    48.842  40.080   9.054  1.00 34.00      C2
ATOM  3478 OE1 GLN  S08    50.031  40.346   9.161  1.00 38.32      C2
ATOM  3479 NE2 GLN  S08    48.321  39.090   9.748  1.00 36.30      C2
ATOM  3480 HE21 GLN  S08   47.373  38.880   9.639  1.00  0.00      C2
ATOM  3481 HE22 GLN  S08   48.891  38.636  10.406  1.00  0.00      C2
ATOM  3482 C   GLN  S08    45.105  43.123   9.111  1.00 24.24      C2
ATOM  3483 O   GLN  S08    43.978  42.650   9.014  1.00 24.06      C2
ATOM  3484 N   LEU  S09    45.375  44.019  10.090  1.00 26.07      C2
ATOM  3485 H   LEU  S09    46.316  44.262  10.222  1.00  0.00      C2
ATOM  3486 CA  LEU  S09    44.378  44.640  10.977  1.00 25.71      C2
ATOM  3487 CB  LEU  S09    44.993  45.555  12.031  1.00 25.60      C2
ATOM  3488 CG  LEU  S09    45.838  44.757  13.042  1.00 29.00      C2
ATOM  3489 CD1 LEU  S09    46.658  45.705  13.886  1.00 28.93      C2
ATOM  3490 CD2 LEU  S09    44.950  43.919  13.937  1.00 27.94      C2
ATOM  3491 C   LEU  S09    43.465  45.471  10.130  1.00 25.17      C2
ATOM  3492 O   LEU  S09    42.274  45.411  10.408  1.00 27.22      C2
ATOM  3493 N   ASP  S10    43.899  46.208   9.101  1.00 23.77      C2
ATOM  3494 H   ASP  S10    44.865  46.277   8.930  1.00  0.00      C2
ATOM  3495 CA  ASP  S10    42.955  46.898   8.240  1.00 22.66      C2
ATOM  3496 CB  ASP  S10    43.652  47.829   7.306  1.00 25.21      C2
ATOM  3497 CG  ASP  S10    44.316  48.966   8.068  1.00 33.01      C2
ATOM  3498 OD1 ASP  S10    45.178  49.621   7.477  1.00 34.28      C2
ATOM  3499 OD2 ASP  S10    43.988  49.209   9.250  1.00 34.44      C2
ATOM  3500 C   ASP  S10    42.104  45.980   7.398  1.00 23.72      C2
ATOM  3501 O   ASP  S10    40.897  46.220   7.387  1.00 24.80      C2
ATOM  3502 N   VAL  S11    42.632  44.984   6.659  1.00 22.38      C2
ATOM  3503 H   VAL  S11    43.611  44.900   6.620  1.00  0.00      C2
ATOM  3504 CA  VAL  S11    41.823  44.010   5.961  1.00 21.89      C2
ATOM  3505 CB  VAL  S11    42.752  42.924   5.366  1.00 22.71      C2
ATOM  3506 CG1 VAL  S11    41.954  41.756   4.792  1.00 20.43      C2
ATOM  3507 CG2 VAL  S11    43.529  43.524   4.210  1.00 16.19      C2
ATOM  3508 C   VAL  S11    40.827  43.403   6.960  1.00 21.92      C2
ATOM  3509 O   VAL  S11    39.625  43.447   6.719  1.00 23.46      C2
ATOM  3510 N   ALA  S12    41.258  43.017   8.163  1.00 20.49      C2
ATOM  3511 H   ALA  S12    42.216  43.063   8.361  1.00  0.00      C2
ATOM  3512 CA  ALA  S12    40.388  42.357   9.108  1.00 20.83      C2
ATOM  3513 CB  ALA  S12    41.103  41.974  10.344  1.00 17.89      C2
ATOM  3514 C   ALA  S12    39.250  43.205   9.550  1.00 23.89      C2
ATOM  3515 O   ALA  S12    38.201  42.668   9.874  1.00 24.61      C2
ATOM  3516 N   ASP  S13    39.417  44.539   9.544  1.00 25.96      C2
ATOM  3517 H   ASP  S13    40.300  44.888   9.291  1.00  0.00      C2
ATOM  3518 CA  ASP  S13    38.374  45.471   9.947  1.00 25.37      C2
ATOM  3519 CB  ASP  S13    38.958  46.787  10.373  1.00 26.88      C2
ATOM  3520 CG  ASP  S13    39.682  46.679  11.712  1.00 32.35      C2
ATOM  3521 OD1 ASP  S13    40.371  47.644  12.058  1.00 35.06      C2
ATOM  3522 OD2 ASP  S13    39.580  45.646  12.390  1.00 34.10      C2
ATOM  3523 C   ASP  S13    37.392  45.730   8.846  1.00 24.95      C2
ATOM  3524 O   ASP  S13    36.185  45.868   9.090  1.00 26.92      C2
ATOM  3525 N   PHE  S14    37.867  45.739   7.634  1.00 22.88      C2
ATOM  3526 H   PHE  S14    38.829  45.614   7.475  1.00  0.00      C2
ATOM  3527 CA  PHE  S14    36.974  45.922   6.530  1.00 24.09      C2
ATOM  3528 CB  PHE  S14    37.812  46.061   5.266  1.00 18.11      C2
ATOM  3529 CG  PHE  S14    36.956  46.470   4.072  1.00 17.86      C2
ATOM  3530 CD1 PHE  S14    35.715  47.089   4.245  1.00 15.18      C2
ATOM  3531 CD2 PHE  S14    37.440  46.197   2.804  1.00 13.77      C2
ATOM  3532 CE1 PHE  S14    34.983  47.419   3.130  1.00 14.53      C2
ATOM  3533 CE2 PHE  S14    36.693  46.539   1.705  1.00 12.10      C2
ATOM  3534 CZ  PHE  S14    35.468  47.146   1.868  1.00 10.68      C2
ATOM  3535 C   PHE  S14    36.026  44.703   6.450  1.00 29.23      C2
ATOM  3536 O   PHE  S14    34.788  44.828   6.350  1.00 29.80      C2
ATOM  3537 N   ALA  S15    36.604  43.490   6.531  1.00 31.15      C2
ATOM  3538 H   ALA  S15    37.581  43.450   6.639  1.00  0.00      C2
ATOM  3539 CA  ALA  S15    35.839  42.260   6.416  1.00 32.36      C2
ATOM  3540 CB  ALA  S15    36.851  41.126   6.402  1.00 32.35      C2
ATOM  3541 C   ALA  S15    34.801  42.089   7.535  1.00 32.39      C2
ATOM  3542 O   ALA  S15    33.676  41.609   7.331  1.00 32.63      C2
ATOM  3543 N   THR  S16    35.164  42.457   8.735  1.00 33.01      C2
ATOM  3544 H   THR  S16    36.117  42.578   8.935  1.00  0.00      C2
ATOM  3545 CA  THR  S16    34.231  42.566   9.821  1.00 35.18      C2
ATOM  3546 CB  THR  S16    35.016  43.018  10.988  1.00 35.40      C2
ATOM  3547 OG1 THR  S16    35.685  41.818  11.336  1.00 42.65      C2
ATOM  3548 HG1 THR  S16    36.505  41.713  10.816  1.00  0.00      C2
ATOM  3549 CG2 THR  S16    34.262  43.672  12.097  1.00 35.56      C2
ATOM  3550 C   THR  S16    33.140  43.554   9.482  1.00 37.62      C2
ATOM  3551 O   THR  S16    32.005  43.315   9.857  1.00 40.57      C2
ATOM  3552 N   THR  S17    33.387  44.666   8.802  1.00 38.61      C2
ATOM  3553 H   THR  S17    34.291  44.850   8.469  1.00  0.00      C2
ATOM  3554 CA  THR  S17    32.359  45.641   8.512  1.00 38.92      C2
ATOM  3555 CB  THR  S17    33.123  46.903   7.962  1.00 40.46      C2
ATOM  3556 OG1 THR  S17    33.832  47.429   9.103  1.00 43.22      C2
ATOM  3557 HG1 THR  S17    34.536  46.815   9.335  1.00  0.00      C2
ATOM  3558 CG2 THR  S17    32.232  47.926   7.253  1.00 39.90      C2
ATOM  3559 C   THR  S17    31.343  45.012   7.551  1.00 38.30      C2
ATOM  3560 O   THR  S17    30.137  45.125   7.811  1.00 38.69      C2
ATOM  3561 N   ILE  S18    31.790  44.344   6.466  1.00 37.54      C2
ATOM  3562 H   ILE  S18    32.756  44.386   6.297  1.00  0.00      C2
ATOM  3563 CA  ILE  S18    30.923  43.646   5.510  1.00 36.10      C2
ATOM  3564 CB  ILE  S18    31.699  42.912   4.439  1.00 34.81      C2
ATOM  3565 CG2 ILE  S18    30.703  42.202   3.555  1.00 33.46      C2
ATOM  3566 CG1 ILE  S18    32.623  43.842   3.699  1.00 32.91      C2
ATOM  3567 CD  ILE  S18    32.019  44.700   2.596  1.00 34.89      C2
ATOM  3568 C   ILE  S18    30.172  42.591   6.317  1.00 38.63      C2
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FIGURE 5

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ATOM  3569 O   ILE 518    28.938  4..45   6.205  1.00 39.93      C2
ATOM  3570 N   TRP 519    30.842  41.785  7.179  1.00 38.64      C2
ATOM  3571 H   TRP 519    31.785  41.959  7.361  1.00  0.00      C2
ATOM  3572 CA  TRP 519    30.144  40.784  7.945  1.00 38.15      C2
ATOM  3573 CB  TRP 519    31.124  40.083  8.780  1.00 38.52      C2
ATOM  3574 CG  TRP 519    30.493  38.793  9.255  1.00 42.26      C2
ATOM  3575 CD2 TRP 519    29.880  38.578  10.473  1.00 41.70     C2
ATOM  3576 CE2 TRP 519    29.437  37.278  10.335  1.00 41.69     C2
ATOM  3577 CE3 TRP 519    29.648  39.282  11.629  1.00 42.26     C2
ATOM  3578 CD1 TRP 519    30.448  37.695  8.419  1.00 42.92      C2
ATOM  3579 NE1 TRP 519    29.788  36.793  9.115  1.00 44.19      C2
ATOM  3580 HE1 TRP 519    29.485  35.935  8.741  1.00  0.00      C2
ATOM  3581 CZ2 TRP 519    28.753  36.671  11.360  1.00 41.91     C2
ATOM  3582 CZ3 TRP 519    28.964  38.666  12.652  1.00 41.77     C2
ATOM  3583 CH2 TRP 519    28.522  37.375  12.515  1.00 41.05     C2
ATOM  3584 C   TRP 519    29.027  41.368  8.815  1.00 39.33      C2
ATOM  3585 O   TRP 519    27.888  40.919  8.726  1.00 38.28      C2
ATOM  3586 N   GLN 520    29.264  42.375  9.650  1.00 41.86      C2
ATOM  3587 H   GLN 520    30.180  42.717  9.700  1.00  0.00      C2
ATOM  3588 CA  GLN 520    28.240  43.016  10.464  1.00 44.63     C2
ATOM  3589 CB  GLN 520    28.691  44.198  11.239  1.00 47.03     C2
ATOM  3590 CG  GLN 520    29.602  43.808  12.360  1.00 54.78     C2
ATOM  3591 CD  GLN 520    29.910  45.009  13.243  1.00 60.14     C2
ATOM  3592 OE1 GLN 520    28.988  45.566  13.854  1.00 61.62     C2
ATOM  3593 NE2 GLN 520    31.172  45.456  13.371  1.00 60.46     C2
ATOM  3594 HE21 GLN 520   31.289  46.260  13.910  1.00  0.00     C2
ATOM  3595 HE22 GLN 520   31.895  44.966  12.932  1.00  0.00     C2
ATOM  3596 C   GLN 520    27.141  43.577  9.621  1.00 46.28      C2
ATOM  3597 O   GLN 520    26.001  43.474  10.059  1.00 48.62     C2
ATOM  3598 N   GLN 521    27.362  44.145  8.442  1.00 46.99      C2
ATOM  3599 H   GLN 521    28.272  44.257  8.092  1.00  0.00      C2
ATOM  3600 CA  GLN 521    26.226  44.638  7.716  1.00 49.02      C2
ATOM  3601 CB  GLN 521    26.632  45.553  6.566  1.00 50.06      C2
ATOM  3602 CG  GLN 521    25.456  46.226  5.790  1.00 50.87      C2
ATOM  3603 CD  GLN 521    24.616  47.278  6.534  1.00 51.82      C2
ATOM  3604 OE1 GLN 521    24.864  47.694  7.671  1.00 52.47     C2
ATOM  3605 NE2 GLN 521    23.577  47.776  5.888  1.00 50.36      C2
ATOM  3606 HE21 GLN 521   23.392  47.455  4.987  1.00  0.00     C2
ATOM  3607 HE22 GLN 521   23.044  48.424  6.390  1.00  0.00     C2
ATOM  3608 C   GLN 521    25.454  43.446  7.155  1.00 50.15      C2
ATOM  3609 O   GLN 521    24.214  43.514  7.177  1.00 51.82      C2
ATOM  3610 N   MET 522    26.057  42.348  6.668  1.00 49.18      C2
ATOM  3611 H   MET 522    27.038  42.291  6.688  1.00  0.00      C2
ATOM  3612 CA  MET 522    25.280  41.227  6.171  1.00 48.22      C2
ATOM  3613 CB  MET 522    26.185  40.167  5.607  1.00 46.36      C2
ATOM  3614 CG  MET 522    26.942  40.661  4.412  1.00 44.32      C2
ATOM  3615 SD  MET 522    27.855  39.435  3.426  1.00 48.35      C2
ATOM  3616 CE  MET 522    28.795  38.447  4.565  1.00 42.80      C2
ATOM  3617 C   MET 522    24.453  40.642  7.316  1.00 50.14      C2
ATOM  3618 O   MET 522    23.380  40.124  7.038  1.00 50.60      C2
ATOM  3619 N   GLU 523    24.848  40.722  8.596  1.00 51.91      C2
ATOM  3620 .1  GLU 523    25.766  41.031  8.769  1.00  0.00      C2
ATOM  3621 CA  GLU 523    24.027  40.313  9.718  1.00 54.53      C2
ATOM  3622 CB  GLU 523    24.654  40.486  11.081  1.00 54.60     C2
ATOM  3623 CG  GLU 523    25.732  39.525  11.398  1.00 57.05     C2
ATOM  3624 CD  GLU 523    25.386  38.150  10.888  1.00 61.72     C2
ATOM  3625 OE1 GLU 523    24.515  37.487  11.477  1.00 64.66     C2
ATOM  3626 OE2 GLU 523    25.979  37.773  9.872  1.00 63.19      C2
ATOM  3627 C   GLU 523    22.773  41.116  9.836  1.00 58.29      C2
ATOM  3628 O   GLU 523    21.688  40.538  9.850  1.00 59.32      C2
ATOM  3629 N   ALA 524    22.920  42.432  9.992  1.00 61.41      C2
ATOM  3630 H   ALA 524    23.834  42.798  10.024  1.00  0.00     C2
ATOM  3631 CA  ALA 524    21.815  43.360  10.076  1.00 63.58     C2
ATOM  3632 CB  ALA 524    22.382  44.768  9.992  1.00 64.11      C2
ATOM  3633 C   ALA 524    20.818  43.109  8.946  1.00 64.79      C2
ATOM  3634 O   ALA 524    19.655  42.824  9.206  1.00 65.69      C2
ATOM  3635 N   ALA 525    21.251  43.083  7.693  1.00 66.44      C2
ATOM  3636 H   ALA 525    22.196  43.283  7.516  1.00  0.00      C2
ATOM  3637 CA  ALA 525    20.371  42.789  6.574  1.00 68.58     C2
ATOM  3638 CB  ALA 525    21.117  43.044  5.288  1.00 67.42      C2
ATOM  3639 C   ALA 525    19.841  41.356  6.558  1.00 71.11      C2
ATOM  3640 O   ALA 525    19.116  40.946  5.651  1.00 71.65      C2
ATOM  3641 N   GLY 526    20.257  40.510  7.498  1.00 74.20      C2
ATOM  3642 H   GLY 526    21.019  40.780  8.043  1.00  0.00      C2
ATOM  3643 CA  GLY 526    19.728  39.157  7.653  1.00 76.50      C2
ATOM  3644 C   GLY 526    20.430  38.085  6.842  1.00 78.19      C2
ATOM  3645 O   GLY 526    20.174  36.910  7.094  1.00 79.05      C2
ATOM  3646 N   MET 527    21.388  38.433  5.970  1.00 80.23      C2
ATOM  3647 H   MET 527    21.759  39.337  6.075  1.00  0.00      C2
ATOM  3648 CA  MET 527    22.055  37.489  5.063  1.00 81.73      C2
ATOM  3649 CB  MET 527    22.771  38.256  3.928  1.00 81.72      C2
ATOM  3650 CG  MET 527    22.385  39.719  3.720  1.00 83.52      C2
ATOM  3651 SD  MET 527    23.364  40.523  2.436  1.00 87.64      C2
ATOM  3652 CE  MET 527    22.600  42.117  2.402  1.00 84.47      C2
ATOM  3653 C   MET 527    23.078  36.584  5.780  1.00 82.64      C2
ATOM  3654 OT1 MET 527    22.974  35.357  5.624  1.00 83.38     C2
ATOM  3655 OT2 MET 527    23.949  37.104  6.500  1.00 82.99     C2
ATOM  3656 CB  MET 538    47.224  28.531  2.401  1.00 77.43      C3
ATOM  3657 CG  MET 538    47.397  30.041  2.427  1.00 77.15      C3
ATOM  3658 SD  MET 538    46.205  30.708  3.604  1.00 79.03      C3
ATOM  3659 CE  MET 538    44.850  31.067  2.515  1.00 77.20      C3
ATOM  3660 C   MET 538    48.549  27.839  0.386  1.00 75.32      C3
ATOM  3661 O   MET 538    49.130  26.745  0.405  1.00 77.11      C3
ATOM  3662 HT1 MET 538    47.563  26.068  1.449  1.00  0.00     C3
ATOM  3663 HT2 MET 538    46.638  26.204  0.075  1.00  0.00     C3
ATOM  3664 N   MET 538    46.724  26.552  1.050  1.00 77.52      C3
ATOM  3665 HT3 MET 538    45.873  26.401  1.617  1.00  0.00     C3
ATOM  3666 CA  MET 538    47.153  27.940  0.995  1.00 76.57      C3
ATOM  3667 N   PRO 539    49.089  28.870 -0.224  1.00 72.65      C3
ATOM  3668 CD  PRO 539    48.346  29.821 -1.046  1.00 72.26      C3
ATOM  3669 CA  PRO 539    50.526  29.020 -0.349  1.00 70.34      C3
ATOM  3670 CB  PRO 539    50.677  30.465 -1.006  1.00 71.89      C3
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FIGURE 5

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ATOM  3671 CG  PRO  539      49.437  30.503  -1.837  1.00 71.52      C3
ATOM  3672 C   PRO  539      51.250  28.931   0.991  1.00 67.83      C3
ATOM  3673 O   PRO  539      50.666  29.294   2.029  1.00 68.05      C3
ATOM  3674 N   ALA  540      52.484  28.417   0.961  1.00 64.48      C3
ATOM  3675 H   ALA  540      52.858  28.098   0.111  1.00  0.00      C3
ATOM  3676 CA  ALA  540      53.389  28.498   2.112  1.00 61.83      C3
ATOM  3677 CB  ALA  540      54.004  27.200   2.619  1.00 63.57      C3
ATOM  3678 C   ALA  540      54.559  29.212   1.496  1.00 58.74      C3
ATOM  3679 O   ALA  540      54.835  29.036   0.301  1.00 58.30      C3
ATOM  3680 N   PHE  541      55.256  30.008   2.292  1.00 55.25      C3
ATOM  3681 H   PHE  541      55.093  30.068   3.257  1.00  0.00      C3
ATOM  3682 CA  PHE  541      56.299  30.814   1.702  1.00 51.38      C3
ATOM  3683 CB  PHE  541      55.964  32.306   1.942  1.00 48.80      C3
ATOM  3684 CG  PHE  541      54.789  32.703   1.058  1.00 45.77      C3
ATOM  3685 CD1 PHE  541      54.992  32.939  -0.279  1.00 44.20      C3
ATOM  3686 CD2 PHE  541      53.507  32.747   1.582  1.00 44.76      C3
ATOM  3687 CE1 PHE  541      53.901  33.207  -1.074  1.00 43.98      C3
ATOM  3688 CE2 PHE  541      52.428  33.018   0.769  1.00 42.86      C3
ATOM  3689 CZ  PHE  541      52.625  33.247  -0.563  1.00 42.52      C3
ATOM  3690 C   PHE  541      57.586  30.364   2.333  1.00 49.80      C3
ATOM  3691 O   PHE  541      58.002  30.807   3.395  1.00 49.55      C3
ATOM  3692 N   ALA  542      58.172  29.442   1.562  1.00 48.21      C3
ATOM  3693 H   ALA  542      57.825  29.298   0.656  1.00  0.00      C3
ATOM  3694 CA  ALA  542      59.326  28.711   1.968  1.00 45.37      C3
ATOM  3695 CB  ALA  542      59.700  27.749   0.898  1.00 45.21      C3
ATOM  3696 C   ALA  542      60.510  29.567   2.266  1.00 44.87      C3
ATOM  3697 O   ALA  542      61.001  29.504   3.374  1.00 46.49      C3
ATOM  3698 N   SER  543      61.013  30.408   1.395  1.00 42.63      C3
ATOM  3699 H   SER  543      60.477  30.685   0.630  1.00  0.00      C3
ATOM  3700 CA  SER  543      62.253  31.108   1.708  1.00 40.31      C3
ATOM  3701 CB  SER  543      63.170  30.861   0.587  1.00 37.74      C3
ATOM  3702 OG  SER  543      62.391  31.181  -0.554  1.00 35.74      C3
ATOM  3703 HG  SER  543      61.824  30.423  -0.751  1.00  0.00      C3
ATOM  3704 C   SER  543      62.087  32.613   1.896  1.00 40.88      C3
ATOM  3705 O   SER  543      61.016  33.115   1.536  1.00 42.63      C3
ATOM  3706 N   ALA  544      63.120  33.383   2.310  1.00 38.84      C3
ATOM  3707 H   ALA  544      63.929  32.951   2.650  1.00  0.00      C3
ATOM  3708 CA  ALA  544      63.035  34.836   2.345  1.00 37.31      C3
ATOM  3709 CB  ALA  544      64.340  35.450   2.808  1.00 35.74      C3
ATOM  3710 C   ALA  544      62.723  35.372   0.947  1.00 37.06      C3
ATOM  3711 O   ALA  544      61.829  36.220   0.820  1.00 38.23      C3
ATOM  3712 N   PHE  545      63.357  34.881  -0.130  1.00 35.72      C3
ATOM  3713 H   PHE  545      64.131  34.298  -0.010  1.00  0.00      C3
ATOM  3714 CA  PHE  545      62.992  35.268  -1.484  1.00 33.66      C3
ATOM  3715 CB  PHE  545      63.738  34.534  -2.593  1.00 29.71      C3
ATOM  3716 CG  PHE  545      63.140  34.742  -3.990  1.00 29.62      C3
ATOM  3717 CD1 PHE  545      62.317  33.788  -4.557  1.00 29.80      C3
ATOM  3718 CD2 PHE  545      63.371  35.915  -4.689  1.00 31.90      C3
ATOM  3719 CE1 PHE  545      61.723  33.984  -5.795  1.00 28.61      C3
ATOM  3720 CE2 PHE  545      62.777  36.113  -5.928  1.00 31.00      C3
ATOM  3721 CZ  PHE  545      61.955  35.150  -6.480  1.00 31.01      C3
ATOM  3722 C   PHE  545      61.543  34.900  -1.667  1.00 34.81      C3
ATOM  3723 O   PHE  545      60.901  35.660  -2.389  1.00 38.88      C3
ATOM  3724 N   GLN  546      60.912  33.847  -1.135  1.00 34.77      C3
ATOM  3725 H   GLN  546      61.396  33.223  -0.558  1.00  0.00      C3
ATOM  3726 CA  GLN  546      59.490  33.637  -1.433  1.00 33.72      C3
ATOM  3727 CB  GLN  546      59.145  32.232  -1.140  1.00 34.85      C3
ATOM  3728 CG  GLN  546      59.582  31.585  -2.444  1.00 42.45      C3
ATOM  3729 CD  GLN  546      59.374  30.085  -2.473  1.00 46.05      C3
ATOM  3730 OE1 GLN  546      59.287  29.472  -1.399  1.00 48.90      C3
ATOM  3731 NE2 GLN  546      59.339  29.442  -3.644  1.00 47.20      C3
ATOM  3732 HE21 GLN  546      59.476  29.948  -4.472  1.00  0.00      C3
ATOM  3733 HE22 GLN  546      59.154  28.481  -3.609  1.00  0.00      C3
ATOM  3734 C   GLN  546      58.504  34.541  -0.729  1.00 31.62      C3
ATOM  3735 O   GLN  546      57.429  34.850  -1.233  1.00 29.88      C3
ATOM  3736 N   ARG  547      58.907  34.929   0.465  1.00 31.09      C3
ATOM  3737 H   ARG  547      59.750  34.566   0.811  1.00  0.00      C3
ATOM  3738 CA  ARG  547      58.160  35.830   1.282  1.00 31.43      C3
ATOM  3739 CB  ARG  547      58.813  35.874   2.601  1.00 31.74      C3
ATOM  3740 CG  ARG  547      57.906  35.224   3.623  1.00 37.02      C3
ATOM  3741 CD  ARG  547      58.344  33.858   4.076  1.00 40.56      C3
ATOM  3742 NE  ARG  547      59.743  34.058   4.345  1.00 47.90      C3
ATOM  3743 HE  ARG  547      60.389  33.924   3.620  1.00  0.00      C3
ATOM  3744 CZ  ARG  547      60.190  34.394   5.543  1.00 49.48      C3
ATOM  3745 NH1 ARG  547      59.361  34.522   6.593  1.00 51.97      C3
ATOM  3746 HH11 ARG  547      58.380  34.356   6.488  1.00  0.00      C3
ATOM  3747 HH12 ARG  547      59.731  34.763   7.493  1.00  0.00      C3
ATOM  3748 NH2 ARG  547      61.464  34.775   5.616  1.00 48.55      C3
ATOM  3749 HH21 ARG  547      62.025  34.803   4.788  1.00  0.00      C3
ATOM  3750 HH22 ARG  547      61.854  35.034   6.501  1.00  0.00      C3
ATOM  3751 C   ARG  547      58.167  37.181   0.590  1.00 32.26      C3
ATOM  3752 O   ARG  547      57.084  37.694   0.317  1.00 34.25      C3
ATOM  3753 N   ARG  548      59.348  37.717   0.205  1.00 31.44      C3
ATOM  3754 H   ARG  548      60.148  37.203   0.444  1.00  0.00      C3
ATOM  3755 CA  ARG  548      59.529  38.980  -0.555  1.00 30.01      C3
ATOM  3756 CB  ARG  548      60.995  39.213  -0.949  1.00 25.42      C3
ATOM  3757 CG  ARG  548      61.820  39.361   0.294  1.00 26.11      C3
ATOM  3758 CD  ARG  548      63.280  39.158  -0.054  1.00 29.34      C3
ATOM  3759 NE  ARG  548      64.044  39.162   1.189  1.00 32.30      C3
ATOM  3760 HE  ARG  548      63.572  38.883   1.995  1.00  0.00      C3
ATOM  3761 CZ  ARG  548      65.344  39.518   1.325  1.00 32.66      C3
ATOM  3762 NH1 ARG  548      66.159  39.923   0.335  1.00 34.98      C3
ATOM  3763 HH11 ARG  548      67.107  40.170   0.543  1.00  0.00      C3
ATOM  3764 HH12 ARG  548      65.812  39.981  -0.600  1.00  0.00      C3
ATOM  3765 NH2 ARG  548      65.837  39.518   2.549  1.00 32.03      C3
ATOM  3766 HH21 ARG  548      66.788  39.783   2.708  1.00  0.00      C3
ATOM  3767 HH22 ARG  548      65.250  39.275   3.321  1.00  0.00      C3
ATOM  3768 C   ARG  548      58.713  38.997  -1.832  1.00 29.81      C3
ATOM  3769 O   ARG  548      57.778  39.790  -1.968  1.00 33.03      C3
ATOM  3770 N   ALA  549      58.979  38.102  -2.761  1.00 27.87      C3
ATOM  3771 H   ALA  549      59.684  37.436  -2.601  1.00  0.00      C3
ATOM  3772 CA  ALA  549      58.227  38.045  -3.984  1.00 27.18      C3
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FIGURE 5

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ATOM  3773 CB  ALA  549     58.797  36.934  -4.857  1.00 28.72      C3
ATOM  3774 C   ALA  549     56.748  37.810  -3.770  1.00 25.91      C3
ATOM  3775 O   ALA  549     55.896  38.337  -4.468  1.00 26.03      C3
ATOM  3776 N   GLY  550     56.421  37.074  -2.748  1.00 26.53      C3
ATOM  3777 H   GLY  550     57.103  36.657  -2.185  1.00  0.00      C3
ATOM  3778 CA  GLY  550     55.055  36.805  -2.457  1.00 26.08      C3
ATOM  3779 C   GLY  550     54.410  38.098  -2.075  1.00 26.94      C3
ATOM  3780 O   GLY  550     53.339  38.380  -2.608  1.00 26.59      C3
ATOM  3781 N   GLY  551     55.073  38.917  -1.234  1.00 27.78      C3
ATOM  3782 H   GLY  551     55.958  38.642  -0.925  1.00  0.00      C3
ATOM  3783 CA  GLY  551     54.540  40.212  -0.779  1.00 26.51      C3
ATOM  3784 C   GLY  551     54.302  41.113  -1.994  1.00 26.82      C3
ATOM  3785 O   GLY  551     53.313  41.852  -2.065  1.00 27.82      C3
ATOM  3786 N   VAL  552     55.154  41.013  -3.012  1.00 25.81      C3
ATOM  3787 H   VAL  552     55.916  40.396  -2.954  1.00  0.00      C3
ATOM  3788 CA  VAL  552     54.952  41.843  -4.176  1.00 28.39      C3
ATOM  3789 CB  VAL  552     56.178  41.743  -5.190  1.00 26.20      C3
ATOM  3790 CG1 VAL  552     55.917  42.391  -6.541  1.00 26.53      C3
ATOM  3791 CG2 VAL  552     57.327  42.546  -4.594  1.00 26.44      C3
ATOM  3792 C   VAL  552     53.650  41.406  -4.820  1.00 29.05      C3
ATOM  3793 O   VAL  552     52.744  42.251  -4.888  1.00 31.68      C3
ATOM  3794 N   LEU  553     53.455  40.120  -5.176  1.00 27.20      C3
ATOM  3795 H   LEU  553     54.122  39.447  -4.908  1.00  0.00      C3
ATOM  3796 CA  LEU  553     52.266  39.705  -5.915  1.00 23.80      C3
ATOM  3797 CB  LEU  553     52.357  38.262  -6.363  1.00 24.86      C3
ATOM  3798 CG  LEU  553     53.432  37.955  -7.357  1.00 23.06      C3
ATOM  3799 CD1 LEU  553     54.073  36.623  -7.092  1.00 24.31      C3
ATOM  3800 CD2 LEU  553     52.794  38.061  -8.703  1.00 21.87      C3
ATOM  3801 C   LEU  553     51.012  39.825  -5.114  1.00 23.72      C3
ATOM  3802 O   LEU  553     49.982  40.138  -5.712  1.00 24.63      C3
ATOM  3803 N   VAL  554     50.962  39.580  -3.803  1.00 24.37      C3
ATOM  3804 H   VAL  554     51.774  39.350  -3.295  1.00  0.00      C3
ATOM  3805 CA  VAL  554     49.660  39.691  -3.180  1.00 26.36      C3
ATOM  3806 CB  VAL  554     49.472  38.751  -1.802  1.00 26.55      C3
ATOM  3807 CG1 VAL  554     50.696  37.933  -1.418  1.00 23.95      C3
ATOM  3808 CG2 VAL  554     48.953  39.614  -0.682  1.00 25.58      C3
ATOM  3809 C   VAL  554     49.322  41.175  -2.960  1.00 27.53      C3
ATOM  3810 O   VAL  554     48.142  41.502  -3.192  1.00 27.44      C3
ATOM  3811 N   ALA  555     50.277  42.106  -2.716  1.00 28.04      C3
ATOM  3812 H   ALA  555     51.221  41.831  -2.658  1.00  0.00      C3
ATOM  3813 CA  ALA  555     49.956  43.539  -2.509  1.00 28.57      C3
ATOM  3814 CB  ALA  555     51.161  44.427  -2.217  1.00 28.07      C3
ATOM  3815 C   ALA  555     49.402  44.055  -3.803  1.00 28.12      C3
ATOM  3816 O   ALA  555     48.425  44.803  -3.847  1.00 30.12      C3
ATOM  3817 N   SER  556     49.985  43.521  -4.839  1.00 26.44      C3
ATOM  3818 H   SER  556     50.781  42.956  -4.710  1.00  0.00      C3
ATOM  3819 CA  SER  556     49.548  43.810  -6.152  1.00 30.09      C3
ATOM  3820 CB  SER  556     50.684  43.277  -6.965  1.00 31.42      C3
ATOM  3821 OG  SER  556     50.442  43.338  -8.344  1.00 37.88      C3
ATOM  3822 HG  SER  556     49.966  44.144  -8.576  1.00  0.00      C3
ATOM  3823 C   SER  556     48.143  43.243  -6.454  1.00 32.78      C3
ATOM  3824 O   SER  556     47.287  43.961  -7.003  1.00 34.56      C3
ATOM  3825 N   HIS  557     47.750  42.019  -6.088  1.00 32.78      C3
ATOM  3826 H   HIS  557     48.350  41.453  -5.560  1.00  0.00      C3
ATOM  3827 CA  HIS  557     46.396  41.605  -6.401  1.00 33.64      C3
ATOM  3828 CB  HIS  557     46.203  40.142  -6.242  1.00 37.88      C3
ATOM  3829 CG  HIS  557     46.986  39.518  -7.348  1.00 42.44      C3
ATOM  3830 CD2 HIS  557     46.694  39.665  -8.675  1.00 43.63      C3
ATOM  3831 ND1 HIS  557     48.108  38.837  -7.209  1.00 45.23      C3
ATOM  3832 HD1 HIS  557     48.641  38.764  -6.385  1.00  0.00      C3
ATOM  3833 CE1 HIS  557     48.524  38.569  -8.414  1.00 46.56      C3
ATOM  3834 NE2 HIS  557     47.676  39.066  -9.283  1.00 45.62      C3
ATOM  3835 HE2 HIS  557     47.793  39.018 -10.257  1.00  0.00      C3
ATOM  3836 C   HIS  557     45.383  42.249  -5.520  1.00 32.94      C3
ATOM  3837 O   HIS  557     44.256  42.444  -5.934  1.00 33.08      C3
ATOM  3838 N   LEU  558     45.744  42.534  -4.280  1.00 33.05      C3
ATOM  3839 H   LEU  558     46.657  42.356  -3.986  1.00  0.00      C3
ATOM  3840 CA  LEU  558     44.817  43.125  -3.348  1.00 31.91      C3
ATOM  3841 CB  LEU  558     45.420  43.107  -1.965  1.00 29.25      C3
ATOM  3842 CG  LEU  558     44.605  43.615  -0.818  1.00 26.02      C3
ATOM  3843 CD1 LEU  558     43.279  42.883  -0.742  1.00 25.00      C3
ATOM  3844 CD2 LEU  558     45.496  43.571   0.408  1.00 22.86      C3
ATOM  3845 C   LEU  558     44.527  44.521  -3.783  1.00 32.47      C3
ATOM  3846 O   LEU  558     43.402  44.944  -3.596  1.00 33.97      C3
ATOM  3847 N   GLN  559     45.482  45.231  -4.370  1.00 34.36      C3
ATOM  3848 H   GLN  559     46.386  44.855  -4.406  1.00  0.00      C3
ATOM  3849 CA  GLN  559     45.255  46.569  -4.912  1.00 36.75      C3
ATOM  3850 CB  GLN  559     46.598  47.067  -5.470  1.00 39.63      C3
ATOM  3851 CG  GLN  559     46.707  48.543  -5.875  1.00 42.07      C3
ATOM  3852 CD  GLN  559     46.530  49.618  -4.793  1.00 41.53      C3
ATOM  3853 OE1 GLN  559     45.961  50.687  -5.057  1.00 41.25      C3
ATOM  3854 NE2 GLN  559     46.951  49.416  -3.561  1.00 37.96      C3
ATOM  3855 HE21 GLN  559     47.271  48.528  -3.311  1.00  0.00      C3
ATOM  3856 HE22 GLN  559     47.001  50.190  -2.967  1.00  0.00      C3
ATOM  3857 C   GLN  559     44.142  46.635  -5.976  1.00 35.22      C3
ATOM  3858 O   GLN  559     43.165  47.404  -5.839  1.00 34.99      C3
ATOM  3859 N   SER  560     44.260  45.817  -7.025  1.00 33.46      C3
ATOM  3860 H   SER  560     45.083  45.292  -7.154  1.00  0.00      C3
ATOM  3861 CA  SER  560     43.222  45.683  -8.049  1.00 32.88      C3
ATOM  3862 CB  SER  560     43.693  44.776  -9.088  1.00 34.05      C3
ATOM  3863 OG  SER  560     45.021  45.174  -9.281  1.00 42.40      C3
ATOM  3864 HG  SER  560     45.042  45.996  -9.783  1.00  0.00      C3
ATOM  3865 C   SER  560     41.885  45.133  -7.559  1.00 32.01      C3
ATOM  3866 O   SER  560     40.791  45.582  -7.920  1.00 32.23      C3
ATOM  3867 N   PHE  561     41.969  44.123  -6.710  1.00 29.50      C3
ATOM  3868 H   PHE  561     42.850  43.767  -6.464  1.00  0.00      C3
ATOM  3869 CA  PHE  561     40.803  43.529  -6.118  1.00 28.17      C3
ATOM  3870 CB  PHE  561     41.237  42.541  -5.040  1.00 26.27      C3
ATOM  3871 CG  PHE  561     40.069  41.966  -4.268  1.00 25.68      C3
ATOM  3872 CD1 PHE  561     39.282  40.999  -4.846  1.00 25.44      C3
ATOM  3873 CD2 PHE  561     39.761  42.482  -3.051  1.00 25.45      C3
ATOM  3874 CE1 PHE  561     38.166  40.551  -4.215  1.00 21.49      C3
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FIGURE 5

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ATOM  3875 CE2 PHE  561     38.635  42.027  -2.421  1.00 26.89      C3
ATOM  3876  CZ PHE  561     37.853  41.074  -3.008  1.00 24.29      C3
ATOM  3877  C  PHE  561     39.987  44.645  -5.505  1.00 28.81      C3
ATOM  3878  O  PHE  561     38.789  44.697  -5.731  1.00 29.31      C3
ATOM  3879  N  LEU  562     40.672  45.565  -4.797  1.00 28.39      C3
ATOM  3880  H  LEU  562     41.643  45.462  -4.707  1.00  0.00      C3
ATOM  3881 CA  LEU  562     40.033  46.617  -4.057  1.00 26.51      C3
ATOM  3882 CB  LEU  562     40.964  47.203  -3.074  1.00 23.80      C3
ATOM  3883 CG  LEU  562     41.047  46.411  -1.816  1.00 24.85      C3
ATOM  3884 CD1 LEU  562     42.207  46.868  -1.049  1.00 24.07      C3
ATOM  3885 CD2 LEU  562     39.794  46.551  -1.008  1.00 25.13      C3
ATOM  3886  C  LEU  562     39.586  47.669  -4.988  1.00 29.27      C3
ATOM  3887  O  LEU  562     38.580  48.304  -4.681  1.00 29.83      C3
ATOM  3888  N  GLU  563     40.239  47.871  -6.115  1.00 30.88      C3
ATOM  3889  H  GLU  563     41.052  47.368  -6.325  1.00  0.00      C3
ATOM  3890 CA  GLU  563     39.738  48.908  -6.966  1.00 36.88      C3
ATOM  3891 CB  GLU  563     40.660  49.142  -8.137  1.00 40.80      C3
ATOM  3892 CG  GLU  563     41.999  49.628  -7.682  1.00 48.55      C3
ATOM  3893 CD  GLU  563     43.148  49.277  -8.619  1.00 55.42      C3
ATOM  3894 OE1 GLU  563     44.301  49.283  -8.135  1.00 57.39      C3
ATOM  3895 OE2 GLU  563     42.886  48.986  -9.808  1.00 56.44      C3
ATOM  3896  C  GLU  563     38.375  48.469  -7.466  1.00 39.02      C3
ATOM  3897  O  GLU  563     37.388  49.170  -7.270  1.00 39.09      C3
ATOM  3898  N  VAL  564     38.289  47.255  -8.030  1.00 42.30      C3
ATOM  3899  H  VAL  564     39.107  46.714  -8.074  1.00  0.00      C3
ATOM  3900 CA  VAL  564     37.052  46.683  -8.558  1.00 41.84      C3
ATOM  3901 CB  VAL  564     37.333  45.255  -9.041  1.00 42.27      C3
ATOM  3902 CG1 VAL  564     36.055  44.538  -9.435  1.00 41.17      C3
ATOM  3903 CG2 VAL  564     38.283  45.348 -10.241  1.00 42.11      C3
ATOM  3904  C  VAL  564     36.030  46.709  -7.442  1.00 41.68      C3
ATOM  3905  O  VAL  564     34.892  47.015  -7.697  1.00 42.34      C3
ATOM  3906  N  SER  565     36.419  46.501  -6.206  1.00 42.75      C3
ATOM  3907  H  SER  565     37.333  46.173  -6.063  1.00  0.00      C3
ATOM  3908 CA  SER  565     35.562  46.602  -5.064  1.00 44.85      C3
ATOM  3909 CB  SER  565     36.344  46.013  -3.894  1.00 46.54      C3
ATOM  3910 OG  SER  565     35.590  45.714  -2.731  1.00 51.75      C3
ATOM  3911 HG  SER  565     35.060  46.481  -2.491  1.00  0.00      C3
ATOM  3912  C  SER  565     35.167  48.063  -4.871  1.00 45.70      C3
ATOM  3913  O  SER  565     34.038  48.287  -4.446  1.00 46.87      C3
ATOM  3914  N  TYR  566     35.965  49.093  -5.146  1.00 47.59      C3
ATOM  3915  H  TYR  566     36.893  48.908  -5.386  1.00  0.00      C3
ATOM  3916 CA  TYR  566     35.518  50.474  -5.086  1.00 49.68      C3
ATOM  3917 CB  TYR  566     36.765  51.362  -5.164  1.00 56.17      C3
ATOM  3918 CG  TYR  566     36.715  52.622  -6.007  1.00 64.64      C3
ATOM  3919 CD1 TYR  566     37.264  52.538  -7.278  1.00 69.53      C3
ATOM  3920 CE1 TYR  566     37.212  53.613  -8.151  1.00 73.71      C3
ATOM  3921 CD2 TYR  566     36.109  53.797  -5.569  1.00 67.98      C3
ATOM  3922 CE2 TYR  566     36.048  54.888  -6.441  1.00 72.92      C3
ATOM  3923  CZ TYR  566     36.599  54.787  -7.735  1.00 75.29      C3
ATOM  3924  OH TYR  566     36.538  55.838  -8.652  1.00 77.42      C3
ATOM  3925  HH TYR  566     36.905  55.565  -9.494  1.00  0.00      C3
ATOM  3926  C  TYR  566     34.524  50.696  -6.217  1.00 48.48      C3
ATOM  3927  O  TYR  566     33.545  51.376  -5.950  1.00 46.35      C3
ATOM  3928  N  ALA  567     34.679  50.115  -7.417  1.00 49.14      C3
ATOM  3929  H  ALA  567     35.512  49.625  -7.572  1.00  0.00      C3
ATOM  3930 CA  ALA  567     33.670  50.165  -8.490  1.00 52.09      C3
ATOM  3931 CB  ALA  567     34.210  49.574  -9.788  1.00 48.37      C3
ATOM  3932  C  ALA  567     32.315  49.449  -8.238  1.00 55.31      C3
ATOM  3933  O  ALA  567     31.226  50.008  -8.501  1.00 56.87      C3
ATOM  3934  N  VAL  568     32.247  48.211  -7.736  1.00 57.66      C3
ATOM  3935  H  VAL  568     33.083  47.729  -7.564  1.00  0.00      C3
ATOM  3936 CA  VAL  568     30.980  47.573  -7.490  1.00 59.61      C3
ATOM  3937 CB  VAL  568     31.119  46.031  -7.339  1.00 58.96      C3
ATOM  3938 CG1 VAL  568     31.239  45.508  -5.911  1.00 60.27      C3
ATOM  3939 CG2 VAL  568     29.851  45.471  -7.922  1.00 60.44      C3
ATOM  3940  C  VAL  568     30.393  48.177  -6.245  1.00 62.66      C3
ATOM  3941  O  VAL  568     29.174  48.154  -6.180  1.00 64.78      C3
ATOM  3942  N  LEU  569     31.075  48.737  -5.248  1.00 66.15      C3
ATOM  3943  H  LEU  569     32.058  48.719  -5.243  1.00  0.00      C3
ATOM  3944 CA  LEU  569     30.359  49.334  -4.123  1.00 69.85      C3
ATOM  3945 CB  LEU  569     31.285  49.858  -3.023  1.00 69.91      C3
ATOM  3946 CG  LEU  569     32.007  48.887  -2.095  1.00 70.17      C3
ATOM  3947 CD1 LEU  569     32.847  49.687  -1.140  1.00 70.19      C3
ATOM  3948 CD2 LEU  569     31.039  48.054  -1.286  1.00 70.56      C3
ATOM  3949  C  LEU  569     29.567  50.509  -4.667  1.00 72.69      C3
ATOM  3950  O  LEU  569     28.365  50.553  -4.425  1.00 73.80      C3
ATOM  3951  N  ARG  570     30.180  51.391  -5.479  1.00 75.95      C3
ATOM  3952  H  ARG  570     31.153  51.299  -5.580  1.00  0.00      C3
ATOM  3953 CA  ARG  570     29.510  52.498  -6.173  1.00 78.78      C3
ATOM  3954 CB  ARG  570     30.399  53.068  -7.308  1.00 80.07      C3
ATOM  3955 CG  ARG  570     29.658  54.222  -7.997  1.00 84.16      C3
ATOM  3956 CD  ARG  570     29.976  54.744  -9.417  1.00 85.66      C3
ATOM  3957 NE  ARG  570     28.892  55.690  -9.737  1.00 85.67      C3
ATOM  3958 HE  ARG  570     27.971  55.354  -9.727  1.00  0.00      C3
ATOM  3959 CZ  ARG  570     29.051  56.991 -10.026  1.00 85.06      C3
ATOM  3960 NH1 ARG  570     30.240  57.590 -10.082  1.00 84.43      C3
ATOM  3961 HH11 ARG  570     31.069  57.056  -9.908  1.00  0.00      C3
ATOM  3962 HH12 ARG  570     30.295  58.561 -10.314  1.00  0.00      C3
ATOM  3963 NH2 ARG  570     27.958  57.736 -10.154  1.00 84.57      C3
ATOM  3964 HH21 ARG  570     27.059  57.316 -10.030  1.00  0.00      C3
ATOM  3965 HH22 ARG  570     28.042  58.708 -10.375  1.00  0.00      C3
ATOM  3966  C  ARG  570     28.201  52.009  -6.812  1.00 79.92      C3
ATOM  3967  O  ARG  570     27.107  52.565  -6.709  1.00 79.61      C3
ATOM  3968  N  HIS  571     28.362  50.900  -7.511  1.00 81.35      C3
ATOM  3969  H  HIS  571     29.214  50.417  -7.440  1.00  0.00      C3
ATOM  3970 CA  HIS  571     27.247  50.306  -8.197  1.00 82.75      C3
ATOM  3971 CB  HIS  571     27.882  49.274  -9.167  1.00 83.42      C3
ATOM  3972 CG  HIS  571     28.633  50.029 -10.280  1.00 85.08      C3
ATOM  3973 CD2 HIS  571     28.921  49.529 -11.532  1.00 85.81      C3
ATOM  3974 ND1 HIS  571     29.074  51.303 -10.268  1.00 86.25      C3
ATOM  3975 HD1 HIS  571     29.080  51.900  -9.489  1.00  0.00      C3
ATOM  3976 CE1 HIS  571     29.595  51.595 -11.439  1.00 86.01      C3
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FIGURE 5

```
ATOM  3977 NE2 HIS  571      29.494  50.518 -12.187  1.00 86.28      C3
ATOM  3978 HE2 HIS  571      29.801  50.468 -13.119  1.00  0.00      C3
ATOM  3979 C   HIS  571      26.225  49.759  -7.195  1.00 83.31      C3
ATOM  3980 O   HIS  571      25.075  50.194  -7.301  1.00 84.06      C3
ATOM  3981 N   LEU  572      26.540  48.963  -6.158  1.00 83.11      C3
ATOM  3982 H   LEU  572      27.474  48.824  -5.915  1.00  0.00      C3
ATOM  3983 CA  LEU  572      25.527  48.457  -5.241  1.00 83.71      C3
ATOM  3984 CB  LEU  572      26.085  47.267  -4.454  1.00 83.57      C3
ATOM  3985 CG  LEU  572      25.439  45.884  -4.721  1.00 83.79      C3
ATOM  3986 CD1 LEU  572      25.783  45.386  -6.127  1.00 84.16      C3
ATOM  3987 CD2 LEU  572      25.958  44.866  -3.714  1.00 84.08      C3
ATOM  3988 C   LEU  572      24.997  49.511  -4.261  1.00 84.78      C3
ATOM  3989 O   LEU  572      24.265  49.192  -3.295  1.00 84.85      C3
ATOM  3990 N   ALA  573      25.349  50.796  -4.483  1.00 85.56      C3
ATOM  3991 H   ALA  573      26.020  50.980  -5.174  1.00  0.00      C3
ATOM  3992 CA  ALA  573      24.822  51.925  -3.721  1.00 85.90      C3
ATOM  3993 CB  ALA  573      25.600  53.207  -3.970  1.00 85.79      C3
ATOM  3994 C   ALA  573      23.373  52.245  -4.057  1.00 87.21      C3
ATOM  3995 OT1 ALA  573      22.610  52.413  -3.099  1.00 88.33      C3
ATOM  3996 OT2 ALA  573      23.022  52.309  -5.248  1.00 88.34      C3
ATOM  3997 OH2 H2O  603      26.735  24.280   5.161  1.00 27.42      W
ATOM  3998 H1  H2O  603      27.332  24.335   4.407  1.00  0.00      W
ATOM  3999 H2  H2O  603      26.288  23.435   4.992  1.00  0.00      W
ATOM  4000 OH2 H2O  605      47.880  37.960  12.073  1.00 56.30      W
ATOM  4001 H1  H2O  605      47.789  37.874  13.031  1.00  0.00      W
ATOM  4002 H2  H2O  605      46.980  37.858  11.753  1.00  0.00      W
ATOM  4003 OH2 H2O  607      40.001  49.224   7.214  1.00 40.04      W
ATOM  4004 H1  H2O  607      40.471  48.761   7.909  1.00  0.00      W
ATOM  4005 H2  H2O  607      40.123  48.642   6.457  1.00  0.00      W
ATOM  4006 OH2 H2O  610      59.883  42.530  -9.698  1.00 38.90      W
ATOM  4007 H1  H2O  610      60.512  41.833  -9.477  1.00  0.00      W
ATOM  4008 H2  H2O  610      59.189  42.046 -10.160  1.00  0.00      W
ATOM  4009 OH2 H2O  611      57.178  35.940 -14.220  1.00 34.63      W
ATOM  4010 H1  H2O  611      57.174  36.545 -14.974  1.00  0.00      W
ATOM  4011 H2  H2O  611      57.989  36.211 -13.757  1.00  0.00      W
ATOM  4012 OH2 H2O  612      25.793  27.337  19.130  1.00 29.21      W
ATOM  4013 H1  H2O  612      26.709  27.661  19.145  1.00  0.00      W
ATOM  4014 H2  H2O  612      25.762  26.792  19.929  1.00  0.00      W
ATOM  4015 OH2 H2O  615      29.766  34.284   9.444  1.00 45.03      W
ATOM  4016 H1  H2O  615      30.017  34.618  10.308  1.00  0.00      W
ATOM  4017 H2  H2O  615      29.113  33.592   9.660  1.00  0.00      W
ATOM  4018 OH2 H2O  617      37.316  40.012  10.872  1.00 35.21      W
ATOM  4019 H1  H2O  617      36.600  40.017  11.519  1.00  0.00      W
ATOM  4020 H2  H2O  617      37.944  39.376  11.259  1.00  0.00      W
ATOM  4021 OH2 H2O  619      40.370  52.041  -7.387  1.00 29.62      W
ATOM  4022 H1  H2O  619      40.672  52.724  -6.779  1.00  0.00      W
ATOM  4023 H2  H2O  619      39.505  51.810  -7.052  1.00  0.00      W
ATOM  4024 OH2 H2O  621      27.903  32.440  10.664  1.00 39.99      W
ATOM  4025 H1  H2O  621      27.553  33.207  11.141  1.00  0.00      W
ATOM  4026 H2  H2O  621      27.929  31.808  11.398  1.00  0.00      W
ATOM  4027 OH2 H2O  622      25.057  31.972  13.675  1.00 32.70      W
ATOM  4028 H1  H2O  622      24.393  32.417  14.215  1.00  0.00      W
ATOM  4029 H2  H2O  622      24.469  31.428  13.112  1.00  0.00      W
ATOM  4030 OH2 H2O  623      20.791  28.583  14.218  1.00 50.17      W
ATOM  4031 H1  H2O  623      20.499  28.803  13.325  1.00  0.00      W
ATOM  4032 H2  H2O  623      19.939  28.549  14.688  1.00  0.00      W
ATOM  4033 OH2 H2O  625      22.680  78.881   2.761  1.00 40.48      W
ATOM  4034 H1  H2O  625      21.938  78.856   3.375  1.00  0.00      W
ATOM  4035 H2  H2O  625      22.266  79.246   1.970  1.00  0.00      W
ATOM  4036 OH2 H2O  626      39.689  36.486   9.730  1.00 23.36      W
ATOM  4037 H1  H2O  626      39.090  35.724   9.672  1.00  0.00      W
ATOM  4038 H2  H2O  626      39.627  36.872   8.853  1.00  0.00      W
ATOM  4039 OH2 H2O  627      42.035  78.320   5.697  1.00 46.19      W
ATOM  4040 H1  H2O  627      42.416  77.450   5.832  1.00  0.00      W
ATOM  4041 H2  H2O  627      41.243  78.146   5.181  1.00  0.00      W
ATOM  4042 OH2 H2O  631      47.227  31.440   6.299  1.00 34.17      W
ATOM  4043 H1  H2O  631      47.533  32.209   5.809  1.00  0.00      W
ATOM  4044 H2  H2O  631      47.442  30.713   5.714  1.00  0.00      W
ATOM  4045 OH2 H2O  636      24.043  65.423  -0.336  1.00 73.38      W
ATOM  4046 H1  H2O  636      24.179  65.781  -1.228  1.00  0.00      W
ATOM  4047 H2  H2O  636      23.469  66.096   0.054  1.00  0.00      W
ATOM  4048 OH2 H2O  638      38.984  67.955 -11.226  1.00 29.97      W
ATOM  4049 H1  H2O  638      38.283  67.402 -11.580  1.00  0.00      W
ATOM  4050 H2  H2O  638      39.568  68.046 -11.998  1.00  0.00      W
ATOM  4051 OH2 H2O  639      27.930  66.675  -7.733  1.00 43.40      W
ATOM  4052 H1  H2O  639      28.192  67.028  -6.876  1.00  0.00      W
ATOM  4053 H2  H2O  639      26.975  66.791  -7.705  1.00  0.00      W
ATOM  4054 OH2 H2O  643      50.619  62.802   0.813  1.00 36.55      W
ATOM  4055 H1  H2O  643      51.575  62.904   0.824  1.00  0.00      W
ATOM  4056 H2  H2O  643      50.301  63.665   0.525  1.00  0.00      W
ATOM  4057 OH2 H2O  646      62.897  38.367   3.759  1.00 73.55      W
ATOM  4058 H1  H2O  646      62.414  38.098   2.978  1.00  0.00      W
ATOM  4059 H2  H2O  646      62.244  38.247   4.461  1.00  0.00      W
ATOM  4060 OH2 H2O  650      29.587  68.480  -9.555  1.00 65.67      W
ATOM  4061 H1  H2O  650      28.846  68.630 -10.148  1.00  0.00      W
ATOM  4062 H2  H2O  650      29.180  67.844  -8.936  1.00  0.00      W
ATOM  4063 OH2 H2O  652      51.408  56.331   4.056  1.00 62.90      W
ATOM  4064 H1  H2O  652      50.718  56.353   3.365  1.00  0.00      W
ATOM  4065 H2  H2O  652      51.052  55.671   4.648  1.00  0.00      W
ATOM  4066 OH2 H2O  653      49.404  56.022   2.161  1.00 51.28      W
ATOM  4067 H1  H2O  653      49.442  55.351   1.474  1.00  0.00      W
ATOM  4068 H2  H2O  653      49.323  56.829   1.630  1.00  0.00      W
ATOM  4069 OH2 H2O  654      68.215  42.294  -2.563  1.00 40.77      W
ATOM  4070 H1  H2O  654      68.347  41.745  -1.777  1.00  0.00      W
ATOM  4071 H2  H2O  654      68.189  43.181  -2.190  1.00  0.00      W
ATOM  4072 OH2 H2O  655      66.374  40.425  -2.489  1.00 42.31      W
ATOM  4073 H1  H2O  655      66.936  41.162  -2.766  1.00  0.00      W
ATOM  4074 H2  H2O  655      66.452  39.841  -3.252  1.00  0.00      W
ATOM  4075 OH2 H2O  656      66.927  41.428  -5.011  1.00 44.08      W
ATOM  4076 H1  H2O  656      66.207  42.071  -4.989  1.00  0.00      W
ATOM  4077 H2  H2O  656      67.542  41.824  -4.474  1.00  0.00      W
ATOM  4078 OH2 H2O  657      40.371  57.111   5.740  1.00 66.56      W
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FIGURE 5

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ATOM  4079 H1  H2O  657    39.958  ...259   5.613  1.00  0.00      W
ATOM  4080 H2  H2O  657    40.021  57.651   5.014  1.00  0.00      W
ATOM  4081 OH2 H2O  658    48.780  47.580  -3.122  1.00 52.09      W
ATOM  4082 H1  H2O  658    48.811  46.671  -3.438  1.00  0.00      W
ATOM  4083 H2  H2O  658    49.568  47.955  -3.542  1.00  0.00      W
ATOM  4084 OH2 H2O  663    29.095  62.889   1.825  1.00 39.23      W
ATOM  4085 H1  H2O  663    29.380  62.827   2.739  1.00  0.00      W
ATOM  4086 H2  H2O  663    28.377  63.526   1.887  1.00  0.00      W
ATOM  4087 OH2 H2O  664    27.132  25.640   7.430  1.00 50.65      W
ATOM  4088 H1  H2O  664    26.870  24.838   7.876  1.00  0.00      W
ATOM  4089 H2  H2O  664    27.001  25.362   6.496  1.00  0.00      W
ATOM  4090 OH2 H2O  665    23.367  30.554  12.167  1.00 49.69      W
ATOM  4091 H1  H2O  665    24.026  30.006  11.707  1.00  0.00      W
ATOM  4092 H2  H2O  665    22.941  31.016  11.438  1.00  0.00      W
ATOM  4093 OH2 H2O  666    46.015  32.192  10.179  1.00 66.86      W
ATOM  4094 H1  H2O  666    46.060  31.519   9.497  1.00  0.00      W
ATOM  4095 H2  H2O  666    45.411  31.827  10.833  1.00  0.00      W
ATOM  4096 OH2 H2O  667    38.943  37.883  11.978  1.00 47.87      W
ATOM  4097 H1  H2O  667    39.367  37.487  11.188  1.00  0.00      W
ATOM  4098 H2  H2O  667    38.521  37.114  12.362  1.00  0.00      W
ATOM  4099 OH2 H2O  671    33.437  58.101   2.269  1.00 46.65      W
ATOM  4100 H1  H2O  671    33.555  57.162   2.433  1.00  0.00      W
ATOM  4101 H2  H2O  671    33.962  58.514   2.961  1.00  0.00      W
ATOM  4102 OH2 H2O  672    27.551  31.314  20.022  1.00 30.15      W
ATOM  4103 H1  H2O  672    27.929  32.042  20.533  1.00  0.00      W
ATOM  4104 H2  H2O  672    26.845  31.764  19.552  1.00  0.00      W
ATOM  4105 OH2 H2O  673    25.714  36.908  21.385  1.00 36.95      W
ATOM  4106 H1  H2O  673    24.806  37.123  21.637  1.00  0.00      W
ATOM  4107 H2  H2O  673    25.599  36.284  20.654  1.00  0.00      W
ATOM  4108 OH2 H2O  674    38.244  66.897  12.076  1.00 57.36      W
ATOM  4109 H1  H2O  674    37.773  67.536  12.626  1.00  0.00      W
ATOM  4110 H2  H2O  674    38.153  66.104  12.618  1.00  0.00      W
ATOM  4111 OH2 H2O  675    35.762  36.553  -3.986  1.00 58.40      W
ATOM  4112 H1  H2O  675    35.600  37.449  -3.677  1.00  0.00      W
ATOM  4113 H2  H2O  675    35.549  36.642  -4.923  1.00  0.00      W
ATOM  4114 OH2 H2O  676    30.689  32.814  25.675  1.00 59.30      W
ATOM  4115 H1  H2O  676    30.093  33.571  25.680  1.00  0.00      W
ATOM  4116 H2  H2O  676    31.550  33.214  25.540  1.00  0.00      W
END
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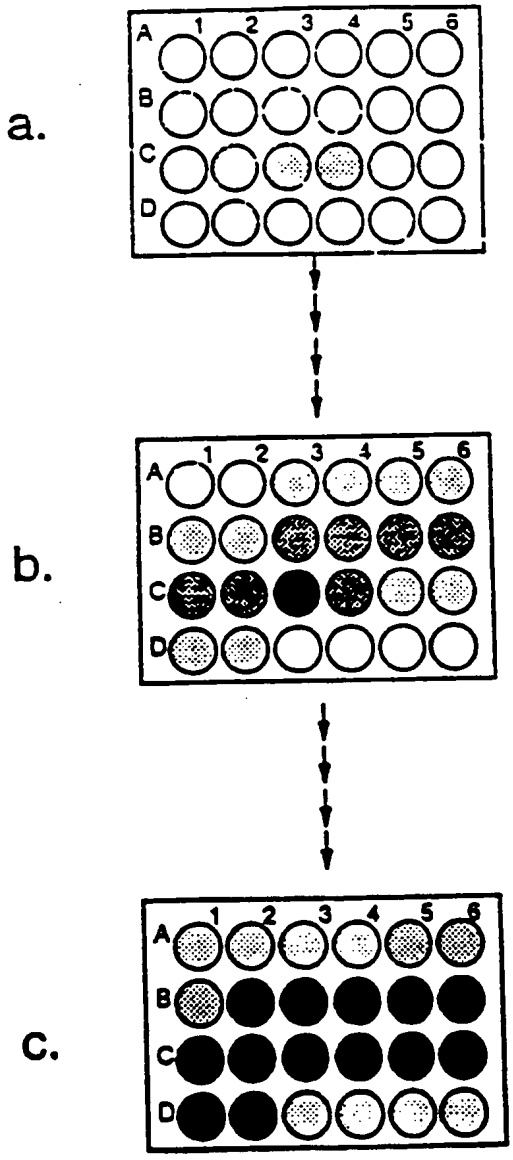

FIGURE 6